

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:30:15 ; Search time 39.8358 Seconds  
(without alignments)  
120.578 Million cell updates/sec

Title: US-09-641-802-2  
Perfect score: 89  
Sequence: 1 LQTPQPLLQVMMEPQGD 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 422553

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	89	100.0	17	4	AAB72501	Aab72501 Colostrin
2	89	100.0	17	4	AAB59310	Aab59310 Ewe colos
3	89	100.0	17	4	AAB72247	Aab72247 Colostrin
4	89	100.0	17	4	AAB72533	Aab72533 Colostrin
5	89	100.0	17	5	AAO14578	Aao14578 Neural ce
6	89	100.0	17	5	AAM51037	Aam51037 Colostrin
7	89	100.0	17	5	AAE20229	Aae20229 Colostrin
8	89	100.0	18	4	AAB59341	Aab59341 Ewe colos
9	56	62.9	11	4	AAE07185	Aae07185 Colostrin

10	56	62.9	12	4	AAE07195	Aae07195	Modified
11	34	38.2	15	5	ABB99038	Abb99038	Carbamyla
12	33	37.1	12	7	ADC44467	Adc44467	Endotheli
13	33	37.1	15	4	AAB72531	Aab72531	Colostrin
14	33	37.1	15	4	AAB59334	Aab59334	Ewe colos
15	33	37.1	15	4	AAB72279	Aab72279	Colostrin
16	33	37.1	15	4	AAB72563	Aab72563	Colostrin
17	33	37.1	15	5	AAO14610	Aao14610	Neural ce
18	33	37.1	15	5	AAM51066	Aam51066	Colostrin
19	33	37.1	15	5	AAE20261	Aae20261	Colostrin
20	32	36.0	8	2	AAR21055	Aar21055	Gamma-car
21	32	36.0	15	6	ABR31148	Abr31148	Human can
22	32	36.0	15	6	ABR31149	Abr31149	Human can
23	32	36.0	15	6	ABR30440	Abr30440	Human can
24	32	36.0	15	6	ABR31517	Abr31517	Human can
25	32	36.0	15	6	ABR30536	Abr30536	Human can
26	32	36.0	15	6	ABR30847	Abr30847	Human can
27	31	34.8	12	3	AAB23189	Aab23189	Hsp47-bin
28	31	34.8	14	4	AAM97279	Aam97279	Human pep
29	31	34.8	15	2	AAW56352	Aaw56352	LO-CD2a l
30	31	34.8	15	2	AAY30191	Aay30191	Framework
31	31	34.8	15	5	AAU74511	Aau74511	Human ATP
32	31	34.8	15	6	ABR38577	Abr38577	Human can
33	31	34.8	15	6	ABR38568	Abr38568	Human can
34	31	34.8	15	6	ABR38729	Abr38729	Human can
35	30	33.7	10	7	ADD15523	Add15523	Predicted
36	30	33.7	14	4	AAM96749	Aam96749	Human pep
37	30	33.7	15	5	AAM47320	Aam47320	Human zin
38	30	33.7	15	6	ABR30169	Abr30169	Human can
39	30	33.7	15	6	ABR30262	Abr30262	Human can
40	30	33.7	15	6	ABR30274	Abr30274	Human can
41	30	33.7	15	6	ABR30229	Abr30229	Human can
42	30	33.7	15	6	ABR30154	Abr30154	Human can
43	30	33.7	15	6	ABR31758	Abr31758	Human can
44	30	33.7	15	6	ABR30297	Abr30297	Human can
45	30	33.7	16	3	AAY65560	Aay65560	Oestrogen
46	30	33.7	16	5	AAU86297	Aau86297	Oestrogen
47	30	33.7	17	4	AAU01845	Aau01845	Wheat pep
48	30	33.7	17	4	AAU01825	Aau01825	Wheat Gli
49	29	32.6	8	6	ABP73085	Abp73085	Amino aci
50	29	32.6	9	5	ABB08361	Abb08361	Synthetic
51	29	32.6	9	7	ABR82213	Abr82213	Human ant
52	29	32.6	10	2	AAY05729	Aay05729	Human G p
53	29	32.6	10	6	ABR05972	Abr05972	Human can
54	29	32.6	10	6	ABR05795	Abr05795	Human can
55	29	32.6	10	6	ABR05791	Abr05791	Human can
56	29	32.6	10	6	ADA14236	Ada14236	Human GPR
57	29	32.6	12	3	AAY92994	Aay92994	Transform
58	29	32.6	12	6	ABU07930	Abu07930	Neisseria
59	29	32.6	13	6	ABP81099	Abp81099	Human TPO
60	29	32.6	15	3	AAY93031	Aay93031	Transform
61	29	32.6	15	3	AAY93032	Aay93032	Transform
62	29	32.6	15	5	ABB09888	Abb09888	N-termina
63	29	32.6	15	6	ABR31395	Abr31395	Human can
64	29	32.6	15	6	ABR30682	Abr30682	Human can
65	29	32.6	15	6	ABR31783	Abr31783	Human can
66	29	32.6	15	6	ABR31394	Abr31394	Human can

67	29	32.6	18	2	AAW66658	Aaw66658	HSV-2 gly
68	29	32.6	18	4	AAM20225	Aam20225	Peptide #
69	29	32.6	18	4	ABB40529	Abb40529	Peptide #
70	29	32.6	18	4	AAM34255	Aam34255	Peptide #
71	29	32.6	18	4	ABB24849	Abb24849	Protein #
72	29	32.6	18	4	AAM74093	Aam74093	Human bon
73	29	32.6	18	4	AAM61355	Aam61355	Human bra
74	29	32.6	18	4	ABG55849	Abg55849	Human liv
75	29	32.6	18	5	ABG43991	Abg43991	Human pep
76	28	31.5	7	2	AAW17515	Aaw17515	Protein k
77	28	31.5	9	7	ADD99989	Add99989	Human 193
78	28	31.5	9	7	ADD99556	Add99556	Human 193
79	28	31.5	9	7	ADD99875	Add99875	Human 193
80	28	31.5	9	7	ADD99363	Add99363	Human 193
81	28	31.5	9	7	ADD99504	Add99504	Human 193
82	28	31.5	9	7	ADD97043	Add97043	Human 193
83	28	31.5	9	7	ADD99343	Add99343	Human 193
84	28	31.5	9	7	ADD98435	Add98435	Human 193
85	28	31.5	9	7	ADD99089	Add99089	Human 193
86	28	31.5	9	7	ADD97071	Add97071	Human 193
87	28	31.5	9	7	ADD98725	Add98725	Human 193
88	28	31.5	9	7	ADD98160	Add98160	Human 193
89	28	31.5	9	7	ADD99400	Add99400	Human 193
90	28	31.5	9	7	ADD99653	Add99653	Human 193
91	28	31.5	9	7	ADD99789	Add99789	Human 193
92	28	31.5	9	7	ADE00025	Ade00025	Human 193
93	28	31.5	9	7	ADD97346	Add97346	Human 193
94	28	31.5	10	4	AAG87925	Aag87925	Saccharom
95	28	31.5	10	7	ADD98298	Add98298	Human 193
96	28	31.5	10	7	ADE00501	Ade00501	Human 193
97	28	31.5	10	7	ADD98062	Add98062	Human 193
98	28	31.5	10	7	ADD98902	Add98902	Human 193
99	28	31.5	10	7	ADD97476	Add97476	Human 193
100	28	31.5	10	7	ADE00482	Ade00482	Human 193

# ALIGNMENTS

## RESULT 1

AAB72501

ID AAB72501 standard; peptide; 17 AA.

XX

AC AAB72501;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #2.

XX

KW Dermatological; oxidative stress regulator; colostrinin.

XX

OS Unidentified.

XX

PN WO200112650-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022665.  
 XX  
 PR 17-AUG-1999; 99US-0149310P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2001-218342/22.  
 XX  
 PT Modulating oxidative stress level in a cell, involves contacting the cell  
 PT with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations.  
 XX  
 PS Claim 6; Page 25; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient  
 XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEPQGD 17  
 |||||  
 Db 1 LQTPQPLLQVMMEPQGD 17

## RESULT 2

AAB59310

ID AAB59310 standard; peptide; 17 AA.

XX

AC AAB59310;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment A-1.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX  
PA (REGE-) REGEN THERAPEUTICS PLC.  
XX  
PI Georgiades JA;  
XX  
DR WPI; 2001-071058/08.  
XX  
PT Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system and  
PT immune system, viral and bacterial infections, and diseases characterized  
PT by amyloid plaques.  
XX  
PS Claim 7; Page 27; 63pp; English.  
XX  
CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques  
XX  
SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEPQGD 17  
| | | | | | | | | | | | | | | | | |  
Db 1 LQTPQPLLQVMMEPQGD 17

# RESULT 3

AAB72247

ID AAB72247 standard; peptide; 17 AA.

XX

AC AAB72247;

XX

DT 14-MAY-2001 (first entry)

XX

DE Colostrinin derived cytokine inducing peptide SEQ ID 2.

XX

KW Colostrinin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological diosrder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.

XX

OS Synthetic.

XX

PN WO200111937-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022818.

XX

PR 17-AUG-1999; 99US-0149311P.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX

DR WPI; 2001-202804/20.

XX

PT Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator.

XX

PS Claim 1; Page 34; 50pp; English.

XX

CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,  
CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
CC have immune response modulatory activity, and are capable of inducing  
CC cytokines. Colostrinin and its derived peptides are useful for inducing  
CC cytokine production, for modulating an immunological response and for  
CC inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.4e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQGD 17

|||||||

Db 1 LQTPQPLLQVMMEPQGD 17

#### RESULT 4

AAB72533

ID AAB72533 standard; peptide; 17 AA.

XX

AC AAB72533;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #2.

XX

KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
KW colostrum.

XX

OS Unidentified.

XX

PN WO200112651-A2.

XX

PD 22-FEB-2001.

XX  
 PF 17-AUG-2000; 2000WO-US022774.  
 XX  
 PR 17-AUG-1999; 99US-0149633P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I;  
 XX  
 DR WPI; 2001-226545/23.  
 XX  
 PT Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating damaged  
 PT neural cells in a patient.  
 XX  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum  
 XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQGD 17  
 |||||  
 Db 1 LQTPQPLLQVMMEPQGD 17

# RESULT 5

AA014578

ID AA014578 standard; peptide; 17 AA.

XX

AC AA014578;

XX

DT 27-MAY-2002 (first entry)

XX

DE Neural cell regulatory colostrinin peptide 2.

XX

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 17

FT /note= "Optional C-terminal amide"

XX

PN WO200213851-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022777.

XX

PR 17-AUG-2000; 2000WO-US022777.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX

PI Boldogh I, Stanton JG, Hughes TK;

XX

DR WPI; 2002-269152/31.

XX

PT Promoting cell differentiation in a patient involves use of blood cell  
PT regulator selected from colostrinin, its constituent peptide and/or  
PT analog.

XX

PS Claim 7; Page 21; 37pp; English.

XX

CC The invention comprises a method for promoting cell differentiation (e.g.  
CC neural cell differentiation). The method involves contacting cells with a  
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
CC polypeptide aggregate that is present in colostrum. The method of the  
CC invention is useful for promoting the differentiation of cells and for  
CC treating damaged neural cells in a patient. The present amino acid  
CC sequence represents a specifically claimed colostrinin peptide used in  
CC the method of the invention

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.4e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQGD 17

|||||

Db 1 LQTPQPLLQVMMEPQGD 17

#### RESULT 6

AAM51037

ID AAM51037 standard; peptide; 17 AA.

XX

AC AAM51037;

XX

DT 30-MAY-2002 (first entry)

XX

DE Colostrinin constituent peptide.

XX

KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
KW blood cell regulator; cytokine inducer; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 17

FT /note= "optional C-terminal amidation"

XX

PN WO200213849-A1.

XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2000; 2000WO-US022775.  
XX  
PR 17-AUG-2000; 2000WO-US022775.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
PA (REGE-) REGEN THERAPEUTICS PLC.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX  
DR WPI; 2002-269150/31.  
XX  
PT Modulation of blood cell proliferation in a patient involves use of blood  
PT cell regulator selected from colostrinin, its constituent peptide and/or  
PT analog.  
XX  
PS Claim 1; Page 34; 54pp; English.  
XX  
CC The present sequence is that of a colostrinin constituent peptide that is  
CC preferred for use as an immunological regulator and as a blood cell  
CC regulator in claimed methods of the invention. Methods are claimed for:  
CC inducing a cytokine in a cell by contact with an immunological regulator,  
CC where the cell is present in a cell culture, a tissue, an organ or an  
CC organism, and the cell is mammalian, including human; modulating an  
CC immune response in a cell by contact with the immunological regulator  
CC under conditions effective to induce a cytokine; modulating an immune  
CC response in a patient by administering an immunological regulator under  
CC conditions effective to induce a cytokine, where the immunological  
CC regulator is administered topically or as part of a dietary supplement,  
CC and where the immune response is specific or non specific, an interferon  
CC response or an antibody response; modulating blood cell proliferation by  
CC contacting blood cells with a blood cell regulator, where the blood cells  
CC are present in a cell culture or an organism, are mammalian or human, and  
CC where the blood cells are increased in number or differentiated; and a  
CC method for modulating blood cell proliferation in a patent. A claimed  
CC cytokine-inducing composition comprises a pharmaceutical carrier and an  
CC active agent such as the present peptide. Cytokines induced by this  
CC peptide in human leucocyte cultures include interferon-gamma, tumour  
CC necrosis factor-alpha, interleukin-4, interleukin-6, interleukin-10 and  
CC interleukin-12. It was one of the best overall inducers in almost all  
CC cytokine and blood cell proliferation experiments conducted  
XX  
SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQGD 17  
| | | | | | | | | | | | | | | | |  
Db 1 LQTPQPLLQVMMEPQGD 17

RESULT 7  
AAE20229

ID AAE20229 standard; peptide; 17 AA.  
 XX  
 AC AAE20229;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide #2.  
 XX  
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnerary.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 17  
 FT /note= "Optionally C-terminal amide"  
 XX  
 PN WO200213850-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US022776.  
 XX  
 PR 17-AUG-2000; 2000WO-US022776.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2002-269151/31.  
 XX  
 PT Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog.  
 XX  
 PS Claim 6; Page 25; 51pp; English.  
 XX  
 CC The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress level  
 CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
 CC organ, or organism; or for treating oxidative damage to the skin of a  
 CC patient e.g. animal or human; to modulate oxidative stress during/ after  
 CC a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQGD 17  
|||||  
Db 1 LQTPQPLLQVMMEPQGD 17

RESULT 8

AAB59341

ID AAB59341 standard; peptide; 18 AA.

XX

AC AAB59341;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment derived sequence #1.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system and  
PT immune system, viral and bacterial infections, and diseases characterized  
PT by amyloid plaques.

XX

PS Claim 8; Page 27; 63pp; English.

XX

CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 89; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.6e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEPQGD 17  
|||||  
Db 2 LQTPQPLLQVMMEPQGD 18

RESULT 9

AAE07185

ID AAE07185 standard; peptide; 11 AA.

XX

AC AAE07185;

XX

DT 06-NOV-2001 (first entry)

XX

DE Colostrinin peptide 1.

XX

KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
KW central nervous system disorder; neurodegenerative disorder; weight loss;  
KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
KW acquired immunological deficiency; neurological disorder; dementia;  
KW antiviral.

XX

OS Unidentified.

XX

PN WO200155199-A1.

XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-GB000329.

XX

PR 26-JAN-2000; 2000GB-00001825.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-488775/53.

XX

PT Peptide useful as an interalia in the treatment of e.g. disorders of the  
PT immune system and the central nervous system comprises ten amino-terminal  
PT amino acid sequence derived from peptides present in colostrinin.

XX

PS Claim 1; Page 15; 40pp; English.

XX

CC The invention relates to colostrinin peptide fragments which are useful,  
CC inter alia, in the treatment of chronic disorders of the immune system  
CC and the central nervous system. Colostrinin peptides are used as a  
CC medicament in the treatment of neurological disorders e.g., dementia,  
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
CC neurosis, in acquired immunological deficiencies, chronic bacterial and

CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxillary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child. The  
 CC present sequence is colostrinin peptide 1 related to the invention  
 XX  
 SQ Sequence 11 AA;

Query Match 62.9%; Score 56; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQ 15  
 |||||  
 Db 1 QPLLQVMMEPQ 11

# RESULT 10

AAE07195

ID AAE07195 standard; peptide; 12 AA.

XX

AC AAE07195;

XX

DT 06-NOV-2001 (first entry)

XX

DE Modified colostrinin cyclic peptide #1.

XX

KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral; cyclic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl; this residue forms a cyclic  
 FT linkage with Gln found at the C-terminal end"

XX

PN WO200155199-A1.

XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-GB000329.

XX

PR 26-JAN-2000; 2000GB-00001825.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX  
 PI Georgiades JA;  
 XX  
 DR WPI; 2001-488775/53.  
 XX  
 PT Peptide useful as an interalia in the treatment of e.g. disorders of the  
 PT immune system and the central nervous system comprises ten amino-terminal  
 PT amino acid sequence derived from peptides present in colostrinin.  
 XX  
 PS Example 2; Page 8; 40pp; English.  
 XX  
 CC The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxillary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child. The  
 CC present sequence is modified colostrinin cyclic peptide #1 related to the  
 CC invention  
 XX  
 SQ Sequence 12 AA;

Query Match 62.9%; Score 56; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.032;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQ 15  
 |||||  
 Db 2 QPLLQVMMEPQ 12

# RESULT 11

ABB99038

ID ABB99038 standard; peptide; 15 AA.

XX

AC ABB99038;

XX

DT 24-JAN-2003 (first entry)

XX

DE Carbamylaspartic dehydrase 9.68 N-terminal amino acid sequence.

XX

KW Carbamylaspartic dehydrase 9.68; enzyme; malignant tumour; haemopathy;

KW development disorder; inflammation; human immunodeficiency virus; HIV;

KW infection; immunological disease.

XX

OS Unidentified.  
 XX  
 PN CN1352302-A.  
 XX  
 PD 05-JUN-2002.  
 XX  
 PF 02-NOV-2000; 2000CN-00127191.  
 XX  
 PR 02-NOV-2000; 2000CN-00127191.  
 XX  
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2002-644474/70.  
 XX  
 PT New polypeptide-carbamylaspartic dehydrase 9.68 and polynucleotide  
 PT encoding the polypeptide.  
 XX  
 PS Example 5; Page 18 (disclosure); 31pp; Chinese.  
 XX  
 CC The invention relates to the polypeptide carbamylaspartic dehydrase 9.68,  
 CC the polynucleotides encoding this polypeptide, and a DNA recombination  
 CC process for production of the polypeptide. Also disclosed is the method  
 CC of applying the polypeptide in the treatment of various diseases such as,  
 CC malignant tumours, haemopathy, development disorder, inflammations, human  
 CC immunodeficiency virus (HIV) infection, and immunological diseases. The  
 CC present invention also discloses the antagonist resisting the polypeptide  
 CC and its treatment effect, and the application of the polynucleotides for  
 CC encoding carbamylaspartic dehydrase 9.68. The current sequence represents  
 CC the carbamylaspartic dehydrase 9.68 N-terminal amino acid sequence  
 XX  
 SQ Sequence 15 AA;

Query Match 38.2%; Score 34; DB 5; Length 15;  
 Best Local Similarity 41.7%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TPQPLLQVMMEP 14  
 :|||| :::|  
 Db 4 SPQPLTGALLQP 15

#### RESULT 12

ADC44467

ID ADC44467 standard; peptide; 12 AA.

XX

AC ADC44467;

XX

DT 18-DEC-2003 (first entry)

XX

DE Endothelial cell binding peptide SEQ ID NO:195.

XX

KW endothelial cell binding protein; ECBP; anti-tumour; cytostatic;

KW vasotropic; antipsoriatic; dermatological; ophthalmological;

KW antidiabetic; antiarthritic; vulnerary; antiulcer; antiinflammatory;

KW antibacterial; gynaecological; angiogenesis.

XX  
 OS Synthetic.  
 XX  
 PN WO2003037172-A2.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 01-NOV-2002; 2002WO-US035258.  
 XX  
 PR 01-NOV-2001; 2001US-0334822P.  
 XX  
 PA (GPCB-) GPC BIOTECH INC.  
 XX  
 PI Gyuris J, Lamphere L, Morris AJ, Tsaion K;  
 XX  
 DR WPI; 2003-482072/45.  
 XX  
 PT Novel synthetic or recombinant polypeptide useful for promoting, reducing  
 PT proliferation and/or migration of endothelial cells, and for modulating  
 PT angiogenesis, has endothelial cell binding protein sequences.  
 XX  
 PS Claim 3; SEQ ID NO 195; 126pp; English.  
 XX  
 CC The invention relates to a novel isolated, synthetic or recombinant  
 CC peptide or polypeptide which includes one or more endothelial cell  
 CC binding protein (ECBP) sequences. A peptide of the invention has anti-  
 CC tumour, cytostatic, vasotropic, antipsoriatic, dermatological,  
 CC ophthalmological, antidiabetic, antiarthritic, vulnerary, antiulcer,  
 CC antiinflammatory, antibacterial, and gynaecological activity. The peptide  
 CC is useful for promoting, reducing the proliferation and/or migration of  
 CC endothelial cells, by treating the cells with an ECBP agonist, which is  
 CC preferably the peptide, to promote proliferation and/or migration of the  
 CC treated cells, and for reducing or promoting angiogenesis, by treating  
 CC the cells with an ECBP antagonist, which is preferably the peptide of the  
 CC invention. A peptide of the invention is also useful for manufacturing a  
 CC medicament for promoting angiogenesis, by admixing an ECBP agonist or  
 CC ECBP antagonist to promote or reduce angiogenesis at one or more sites in  
 CC a treated mammal. The medicament is useful for promoting or reducing  
 CC angiogenesis. ECBP sequences are useful to alter the infectivity spectrum  
 CC of a viral particle. The present sequence represents an ECBP of the  
 CC invention.  
 XX  
 SQ Sequence 12 AA;

Query Match 37.1%; Score 33; DB 7; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQP 6  
 |||||  
 Db 2 LQTPQP 7

RESULT 13  
 AAB72531  
 ID AAB72531 standard; peptide; 15 AA.  
 XX

AC AAB72531;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #32.  
 XX  
 KW Dermatological; oxidative stress regulator; colostrinin.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112650-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US022665.  
 XX  
 PR 17-AUG-1999; 99US-0149310P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2001-218342/22.  
 XX  
 PT Modulating oxidative stress level in a cell, involves contacting the cell  
 PT with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations.  
 XX  
 PS Claim 6; Page 26; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient  
 XX  
 SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 4; Length 15;  
 Best Local Similarity 53.8%; Pred. No. 2e+02;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14  
 | | | | : | |  
 Db 3 QPPQPLPPTVMFP 15

RESULT 14  
 AAB59334  
 ID AAB59334 standard; peptide; 15 AA.  
 XX  
 AC AAB59334;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX

DE Ewe colostrinin peptide fragment C-9.  
 XX  
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX  
 PN WO200075173-A2.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 02-JUN-2000; 2000WO-GB002128.  
 XX  
 PR 02-JUN-1999; 99GB-00012852.  
 XX  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA;  
 XX  
 DR WPI; 2001-071058/08.  
 XX  
 PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system and  
 PT immune system, viral and bacterial infections, and diseases characterized  
 PT by amyloid plaques.  
 XX  
 PS Claim 7; Page 27; 63pp; English.  
 XX  
 CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques  
 XX  
 SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 4; Length 15;  
 Best Local Similarity 53.8%; Pred. No. 2e+02;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14  
 | ||| :| |  
 Db 3 QPPQPLPPTVMFP 15

# RESULT 15

AAB72279

ID AAB72279 standard; peptide; 15 AA.

XX

AC AAB72279;

XX

DT 14-MAY-2001 (first entry)

XX

DE Colostrinin derived cytokine inducing peptide SEQ ID 34.

XX  
 KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200111937-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US022818.  
 XX  
 PR 17-AUG-1999; 99US-0149311P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX  
 DR WPI; 2001-202804/20.  
 XX  
 PT Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator.  
 XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
 CC have immune response modulatory activity, and are capable of inducing  
 CC cytokines. Colostrinin and its derived peptides are useful for inducing  
 CC cytokine production, for modulating an immunological response and for  
 CC inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies  
 XX  
 SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 4; Length 15;  
 Best Local Similarity 53.8%; Pred. No. 2e+02;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14  
 | | | | : | |  
 Db 3 QPPQPLPPTVMFP 15

RESULT 16  
 AAB72563  
 ID AAB72563 standard; peptide; 15 AA.  
 XX

AC AAB72563;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #32.  
 XX  
 KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112651-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US022774.  
 XX  
 PR 17-AUG-1999; 99US-0149633P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I;  
 XX  
 DR WPI; 2001-226545/23.  
 XX  
 PT Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating damaged  
 PT neural cells in a patient.  
 XX  
 PS Claim 6; Page 22; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum  
 XX  
 SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 4; Length 15;  
 Best Local Similarity 53.8%; Pred. No. 2e+02;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14  
 | | | | : | |  
 Db 3 QPPQPLPPTVMFP 15

# RESULT 17

AAO14610

ID AAO14610 standard; peptide; 15 AA.

XX

AC AAO14610;

XX

DT 27-MAY-2002 (first entry)

XX

DE Neural cell regulatory colostrinin peptide 32.

XX

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
KW neural cell treatment.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 15

FT /note= "Optional C-terminal amide"

XX

PN WO200213851-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022777.

XX

PR 17-AUG-2000; 2000WO-US022777.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX

PI Boldogh I, Stanton JG, Hughes TK;

XX

DR WPI; 2002-269152/31.

XX

PT Promoting cell differentiation in a patient involves use of blood cell  
PT regulator selected from colostrinin, its constituent peptide and/or  
PT analog.

XX

PS Claim 7; Page 22; 37pp; English.

XX

CC The invention comprises a method for promoting cell differentiation (e.g.  
CC neural cell differentiation). The method involves contacting cells with a  
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
CC polypeptide aggregate that is present in colostrum. The method of the  
CC invention is useful for promoting the differentiation of cells and for  
CC treating damaged neural cells in a patient. The present amino acid  
CC sequence represents a specifically claimed colostrinin peptide used in  
CC the method of the invention

XX

SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 5; Length 15;

Best Local Similarity 53.8%; Pred. No. 2e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14

| | | | : | |

Db 3 QPPQPLPPTVMFP 15

RESULT 18

AAM51066

ID AAM51066 standard; peptide; 15 AA.

XX

AC AAM51066;

XX

DT 30-MAY-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide (casein amino acids 159-173).  
 XX  
 KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; beta-casein; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 15  
 FT /note= "optional C-terminal amidation"  
 XX  
 PN WO200213849-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US022775.  
 XX  
 PR 17-AUG-2000; 2000WO-US022775.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX  
 DR WPI; 2002-269150/31.  
 XX  
 PT Modulation of blood cell proliferation in a patient involves use of blood  
 PT cell regulator selected from colostrinin, its constituent peptide and/or  
 PT analog.  
 XX  
 PS Claim 1; Page 34; 54pp; English.  
 XX  
 CC The present sequence is that of a colostrinin constituent peptide that is  
 CC used as an immunological regulator and as a blood cell regulator in  
 CC claimed methods of the invention. It is classified as having a beta-  
 CC casein homologue precursor, and corresponds to casein amino acids 159-  
 CC 173. Methods are claimed for: inducing a cytokine in a cell by contact  
 CC with an immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is mammalian,  
 CC including human; modulating an immune response in a cell by contact with  
 CC the immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering an  
 CC immunological regulator under conditions effective to induce a cytokine,  
 CC where the immunological regulator is administered topically or as part of  
 CC a dietary supplement, and where the immune response is specific or non  
 CC specific, an interferon response or an antibody response; modulating  
 CC blood cell proliferation by contacting blood cells with a blood cell  
 CC regulator, where the blood cells are present in a cell culture or an  
 CC organism, are mammalian or human, and where the blood cells are increased  
 CC in number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide  
 XX  
 SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 5; Length 15;  
Best Local Similarity 53.8%; Pred. No. 2e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14  
| |||| :| |  
Db 3 QPPQPLPPTVMFP 15

RESULT 19

AAE20261

ID AAE20261 standard; peptide; 15 AA.

XX

AC AAE20261;

XX

DT 18-JUN-2002 (first entry)

XX

DE Colostrinin constituent peptide #32.

XX

KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnerary.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 15

FT /note= "Optionally C-terminal amide"

XX

PN WO200213850-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022776.

XX

PR 17-AUG-2000; 2000WO-US022776.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX

PI Stanton GJ, Hughes TK, Boldogh I;

XX

DR WPI; 2002-269151/31.

XX

PT Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
PT constituent peptide and/or analog.

XX

PS Claim 6; Page 26; 51pp; English.

XX

CC The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress level  
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
CC organ, or organism; or for treating oxidative damage to the skin of a  
CC patient e.g. animal or human; to modulate oxidative stress during/ after

CC a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide

XX

SQ Sequence 15 AA;

Query Match 37.1%; Score 33; DB 5; Length 15;  
 Best Local Similarity 53.8%; Pred. No. 2e+02;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14  
 | |||| :| |  
 Db 3 QPPQPLPPTVMFP 15

# RESULT 20

AAR21055

ID AAR21055 standard; peptide; 8 AA.

XX

AC AAR21055;

XX

DT 25-MAR-2003 (revised)

DT 01-JUN-1992 (first entry)

XX

DE Gamma-carboxylase, N-terminus.

XX

KW Degenerate; Vitamin K dependent proteins; PCR.

XX

OS Homo sapiens.

XX

PN WO9201795-A.

XX

PD 06-FEB-1992.

XX

PF 23-JUL-1990; 90US-00557220.

XX

PR 23-JUL-1990; 90US-00557220.

PR 14-MAR-1991; 91US-00669735.

XX

PA (ZYMO ) ZYMOGENETICS INC.

XX

PI Berkner KL;

XX

DR WPI; 1992-064951/08.

XX

PT Gamma-carboxylase protein compsns. - used in recombinant prodn. of active  
 PT vitamin=K dependent proteins.

XX

PS Claim 6; Table 9; 91pp; English.

XX

CC Nucleotide sequences encoding gamma-carboxylase were obtd. using PCR, and  
CC oligonucleotides designed from amino acid sequences determined by  
CC microsequencing of partially purified material. SEQ ID No 19 (peptide 5)  
CC is one of seven alternative sequences for the N-terminus of gamma  
CC carboxylase, due to the degeneracy of the genetic code. Obtaining the  
CC full DNA and protein sequence of gamma-carboxylase will allow proteins  
CC such as Factor VII, Factor IX, prothrombin, (activated) protein C,  
CC protein S, protein Z, or osteocalcin to be easily produced by recombinant  
CC techniques. See also AAR21049-56, AAR23010. (Updated on 25-MAR-2003 to  
CC correct PA field.)

XX

SQ Sequence 8 AA;

Query Match 36.0%; Score 32; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPQPLL 8

|||||

Db 1 TPQPLL 6

#### RESULT 21

ABR31148

ID ABR31148 standard; peptide; 15 AA.

XX

AC ABR31148;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 83P4B8 HLA peptide #2210.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 487; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 15 AA;

Query Match 36.0%; Score 32; DB 6; Length 15;  
Best Local Similarity 58.3%; Pred. No. 2.9e+02;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMM 12

|: |||:| |

Db 4 LKAVQPLLKVSM 15

#### RESULT 22

ABR31149

ID ABR31149 standard; peptide; 15 AA.

XX

AC ABR31149;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 83P4B8 HLA peptide #2211.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 487; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 15 AA;

Query Match 36.0%; Score 32; DB 6; Length 15;  
Best Local Similarity 58.3%; Pred. No. 2.9e+02;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMM 12

|: ||||:| |

Db 1 LKAVQPLLKVSM 12

#### RESULT 23

ABR30440

ID ABR30440 standard; peptide; 15 AA.

XX

AC ABR30440;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 83P4B8 HLA peptide #1502.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.  
PR 10-APR-2001; 2001US-0283112P.  
PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 475; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 15 AA;

Query Match 36.0%; Score 32; DB 6; Length 15;  
Best Local Similarity 58.3%; Pred. No. 2.9e+02;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMM 12  
|: ||||:| |  
Db 1 LKAVQPLLKVSM 12

#### RESULT 24

ABR31517

ID ABR31517 standard; peptide; 15 AA.

XX

AC ABR31517;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 83P4B8 HLA peptide #2579.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 494; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 15 AA;

Query Match 36.0%; Score 32; DB 6; Length 15;  
 Best Local Similarity 58.3%; Pred. No. 2.9e+02;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMM 12  
 |: ||||:| |  
 Db 1 LKAVQPLLKVSM 12

#### RESULT 25

ABR30536

ID ABR30536 standard; peptide; 15 AA.

XX

AC ABR30536;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 83P4B8 HLA peptide #1598.

XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 476; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 15 AA;

Query Match 36.0%; Score 32; DB 6; Length 15;  
 Best Local Similarity 58.3%; Pred. No. 2.9e+02;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMM 12  
 | : | | | : | |  
 Db 4 LKAVQPLLKVSM 15

RESULT 26  
 ABR30847  
 ID ABR30847 standard; peptide; 15 AA.

XX  
 AC ABR30847;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 83P4B8 HLA peptide #1909.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 482; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 15 AA;  
  
 Query Match 36.0%; Score 32; DB 6; Length 15;  
 Best Local Similarity 58.3%; Pred. No. 2.9e+02;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
 Qy 1 LQTPQPLLQVMM 12  
 |: ||||:| |

## RESULT 27

AAB23189

ID AAB23189 standard; peptide; 12 AA.

XX

AC AAB23189;

XX

DT 29-JAN-2001 (first entry)

XX

DE Hsp47-binding hydrophobic phage display dodecapeptide, SEQ ID NO:11.

XX

KW Hsp47-binding hydrophobic dodecapeptide; phage display library;

KW Hsp47 external domain; carcinoma; cancer; targetting molecule; therapy;

KW diagnosis; detection; imaging; drug delivery; invasion; migration;

KW metastasis; modulation; tumour; skin; basal cells; colon;

KW large intestine; lung; breast; bladder; oral cancer;

KW head and neck cancer; larynx; nasopharynx; adrenal cortex;

KW apocrine gland; kidney; liver; pancreas; prostate.

XX

OS Synthetic.

XX

PN WO200054805-A1.

XX

PD 21-SEP-2000.

XX

PF 15-MAR-2000; 2000WO-US006588.

XX

PR 15-MAR-1999; 99US-0124481P.

XX

PA (UYMA-) UNIV MARYLAND BALTIMORE.

XX

PI Sauk JJ;

XX

DR WPI; 2000-655997/63.

XX

PT Treating, diagnosing or modulating a carcinoma cell, which expresses Heat  
PT shock protein 47 on its surface, involves administering an agent  
PT comprising targeting moiety which binds to Hsp47 external domain.

XX

PS Claim 6; Page 8; 87pp; English.

XX

CC The invention relates to methods of treating and diagnosing carcinomas in  
CC which heat shock protein 47 (Hsp47) is expressed on the surface of the  
CC carcinoma cells, involving administering an agent comprising a targetting  
CC moiety which specifically binds to the external domain of Hsp47. The  
CC invention also relates to peptides (AAB23181-B23203) which specifically  
CC bind to external domains of such surface-localised Hsp47 molecules and  
CC have sequences encompassed by the generic sequences XHyHyXXHyXXXXHyHy or  
CC HyXXXHyHyXXHyXXX where X, independently, can be any amino acid and Hy,  
CC independently, can be any hydrophobic amino acid. The invention also  
CC encompasses methods of screening for agents which bind Hsp47 external  
CC domains. Hsp47-binding agents can be may be used to treat Hsp47-  
CC expressing carcinomas, and for modulating the activity of a tumour cell  
CC with respect to invasion, migration, motility or metastasis, or to its  
CC interaction with the extracellular matrix. The targetting moiety (such as

CC an Hsp47-binding peptide, a toxin or an antibody) may be coupled with a  
 CC therapeutic moiety (such as a cytotoxic agent or a therapeutic gene) for  
 CC cancer treatment, or with a detectable moiety for imaging. Carcinomas  
 CC which may be treated or diagnosed according to methods of the invention  
 CC include those of the skin, basal cells, large intestine, lung, colon,  
 CC breast, bladder, oral, head and neck, larynx, nasopharynx, adrenal  
 CC cortex, apocrine glands, kidney, liver, pancreas, or prostate. Targetting  
 CC carcinoma cells with Hsp47-binding agents results in efficient delivery  
 CC of therapeutic agents, reduced doses, reduced side effects and sensitive  
 CC detection or imaging of carcinoma cells. Sequences AAB23181-B23191  
 CC represent predominantly hydrophobic phage display library dodecapeptides  
 CC identified as being able to bind Hsp47 in an exemplification of the  
 CC invention

XX

SQ Sequence 12 AA;

Query Match 34.8%; Score 31; DB 3; Length 12;  
 Best Local Similarity 41.7%; Pred. No. 3.3e+02;  
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 TPQPLLQVMMEP 14

|||| : : : |

Db 1 TPQPNMMLRISP 12

# RESULT 28

AAM97279

ID AAM97279 standard; peptide; 14 AA.

XX

AC AAM97279;

XX

DT 24-JAN-2002 (first entry)

XX

DE Human peptide #554 encoded by a SNP oligonucleotide.

XX

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.

XX

OS Homo sapiens.

XX

PN WO200147944-A2.

XX

PD 05-JUL-2001.

XX

PF 28-DEC-2000; 2000WO-US035498.

XX

PR 28-DEC-1999; 99US-0173419P.

PR 27-DEC-2000; 2000US-00173419.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA, Leach M;  
 XX  
 DR WPI; 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.  
 XX  
 PS Disclosure; Page 3789; 4143pp; English.  
 XX  
 CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms  
 XX  
 SQ Sequence 14 AA;

Query Match 34.8%; Score 31; DB 4; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PLLQVMME 13  
 ||:| |||  
 Db 1 PLIQEMME 8

# RESULT 29

AAW56352

ID AAW56352 standard; peptide; 15 AA.

XX

AC AAW56352;

XX

DT 17-AUG-1998 (first entry)

XX

DE LO-CD2a light chain framework region 2.

XX

KW LO-CD2a; monoclonal antibody; CD2; rat; chimeric antibody;

KW humanised antibody; antibody engineering; graft rejection;

KW graft versus host disease; autoimmune disease; therapy.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Misc-difference 2

FT /note= "retained in humanised antibody"

FT Misc-difference 3  
 FT /note= "retained in humanised antibody"  
 FT Misc-difference 11  
 FT /note= "retained in humanised antibody"  
 FT Misc-difference 12  
 FT /note= "retained in humanised antibody"  
 XX  
 PN WO9807444-A1.  
 XX  
 PD 26-FEB-1998.  
 XX  
 PF 16-AUG-1996; 96WO-US013281.  
 XX  
 PR 16-AUG-1996; 96WO-US013281.  
 XX  
 PA (BIOT-) BIOTRANSPLANT INC.  
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.  
 XX  
 PI Bazin H, Latinne D, Kaplan R, Kieber-Emmons T, Postema CE;  
 PI White-Scharf ME;  
 XX  
 DR WPI; 1998-168898/15.  
 XX  
 PT Humanised antibody - comprises complementarity determining region from LO  
 PT -CD2a, useful to prevent or inhibit graft versus host or auto-immune  
 PT disease.  
 XX  
 PS Example 7; Page 58; 133pp; English.  
 XX  
 CC This peptide comprises framework region 2 (FR 2) of the light chain (see  
 CC AAW56347) of rat anti-CD2 monoclonal antibody LO-CD2a. FRs 1-4 (see  
 CC AAW56351-54) were compared with FRs 1-4 of the human HUM5400 light chain.  
 CC A novel humanized LO-CD2a light chain (see AAW56349) comprises rat LO-  
 CC CD2a complementarity determining regions and HUM5400 constant regions,  
 CC but with amino acids 9, 12, 41, 42, 50, 51 and 82 of the rat framework  
 CC retained to maintain binding specificity. The chimeric antibody can be  
 CC used to inhibit an immune response, specifically human T cell activation  
 CC and proliferation, in a patient, and to inhibit rejection of a graft in a  
 CC patient (claimed), useful for preventing or inhibiting graft versus host  
 CC or autoimmune disease  
 XX  
 SQ Sequence 15 AA;

Query Match 34.8%; Score 31; DB 2; Length 15;  
 Best Local Similarity 71.4%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8  
 |:|:|:|:  
 Db 8 QSPQPLI 14

RESULT 30  
 AAY30191  
 ID AAY30191 standard; peptide; 15 AA.  
 XX  
 AC AAY30191;

XX  
 DT 29-OCT-1999 (first entry)  
 XX  
 DE Framework 2 region of rat monoclonal antibody LO-CD2a light chain.  
 XX  
 KW Antibody LO-CD2a; CD2 antigen; T-lymphocyte; humanised antibody;  
 KW T-cell-mediated immune response; graft rejection; autoimmune disease;  
 KW graft-versus-host disease; T cell; natural killer cell.  
 XX  
 OS Rattus sp.  
 XX  
 PN US5951983-A.  
 XX  
 PD 14-SEP-1999.  
 XX  
 PF 07-JUN-1995; 95US-00477989.  
 XX  
 PR 05-MAR-1993; 93US-00027008.  
 PR 09-SEP-1993; 93US-00119032.  
 PR 29-MAR-1995; 95US-00407009.  
 XX  
 PA (BIOT-) BIO TRANSPLANT INC.  
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.  
 XX  
 PI White-Scharf ME, Postema CE, Kaplan R, Latinne D, Bazin H;  
 PI Kieber-Emmons T;  
 XX  
 DR WPI; 1999-526991/44.  
 XX  
 PT Antibody mediated Inhibition of T cell immune response.  
 XX  
 PS Example 7; Col 33-34; 104pp; English.  
 XX  
 CC The present sequence represent a framework region of rat monoclonal  
 CC antibody LO-CD2a. LO-CD2a binds to an epitope of a CD2 antigen T-  
 CC lymphocytes. The present sequence is compared to the corresponding region  
 CC from a human V kappa gene, and used to design humanised sequences. The  
 CC humanized LO-CD2a antibody comprises the human constant regions, a light  
 CC chain framework region derived from a human antibody, a heavy chain  
 CC framework region derived from a human antibody, heavy and light chain  
 CC complementarity determining regions (CDRs) of the non-human monoclonal  
 CC antibody produced by the cell line deposited as ATCC HB11423. The  
 CC humanised antibodies are used in a method for treating a patient to  
 CC inhibit a T-cell-mediated immune response. The method is useful for the  
 CC treatment or prevention of graft rejection and graft-versus-host disease,  
 CC as well as in the treatment of autoimmune diseases which are mediated by  
 CC the activation and proliferation of T cells or natural killer cells  
 XX  
 SQ Sequence 15 AA;

Query Match 34.8%; Score 31; DB 2; Length 15;  
 Best Local Similarity 71.4%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8  
 | : | | | :  
 Db 8 QSPQPLI 14

RESULT 31

AAU74511

ID AAU74511 standard; peptide; 15 AA.

XX

AC AAU74511;

XX

DT 09-APR-2002 (first entry)

XX

DE Human ATP dependent serine proteinase 21 N-terminal peptide.

XX

KW Human; ATP dependent serine protease 21; malignant tumour; HIV;  
 KW haemopathy; human immunodeficiency virus; immunological disease;  
 KW inflammation; cytostatic; haemostatic; virucide; immunomodulatory;  
 KW antiinflammatory; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200194529-A2.

XX

PD 13-DEC-2001.

XX

PF 28-APR-2001; 2001WO-CN000658.

XX

PR 29-APR-2000; 2000CN-00115512.

XX

PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-090143/12.

XX

PT Human ATP dependent serine proteinase 21 and encoding polynucleotide,  
 PT used in diagnosis and treatment of malignant tumors, hemopathy, human  
 PT immunodeficiency virus infection, immunological diseases and  
 PT inflammation.

XX

PS Example 5; Page 18; 32pp; Chinese.

XX

CC The invention relates to an isolated polypeptide of human ATP dependent  
 CC serine proteinase 21. The protein of the invention and its associated  
 CC cDNA sequence are used in the treatment of various diseases including  
 CC malignant tumours, haemopathy, human immunodeficiency virus (HIV)  
 CC infection, immunological diseases and various inflammations. This  
 CC sequence represents the N-terminal peptide of ATP dependent serine  
 CC proteinase 21, used in ELISA

XX

SQ Sequence 15 AA;

Query Match 34.8%; Score 31; DB 5; Length 15;

Best Local Similarity 46.2%; Pred. No. 4.1e+02;

Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQGD 17

| | ::|||

Db 3 QLLESTVIQPD 15

RESULT 32

ABR38577

ID ABR38577 standard; peptide; 15 AA.

XX

AC ABR38577;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 192P2G7 HLA peptide #1437.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 622; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 15 AA;

Query Match

34.8%; Score 31; DB 6; Length 15;

Best Local Similarity 46.2%; Pred. No. 4.1e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
|: ||| |:: |  
Db 2 LEYPQPGLDIIKE 14

RESULT 33

ABR38568

ID ABR38568 standard; peptide; 15 AA.

XX

AC ABR38568;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 192P2G7 HLA peptide #1428.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 622; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 15 AA;

Query Match 34.8%; Score 31; DB 6; Length 15;  
Best Local Similarity 46.2%; Pred. No. 4.1e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
|: ||| | :: |  
Db 3 LEYPQPGLDIIKE 15

RESULT 34

ABR38729

ID ABR38729 standard; peptide; 15 AA.

XX

AC ABR38729;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 192P2G7 HLA peptide #1589.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 624; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 15 AA;

Query Match 34.8%; Score 31; DB 6; Length 15;  
Best Local Similarity 46.2%; Pred. No. 4.1e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
|: ||| |::|  
Db 2 LEYPQPGLDIIKE 14

#### RESULT 35

ADD15523

ID ADD15523 standard; peptide; 10 AA.

XX

AC ADD15523;

XX

DT 15-JAN-2004 (first entry)

XX

DE Predicted epitopic region of the S\_aureus GlmM protein (SeqID 88).

XX

KW microbial; antimicrobial; membrane biosynthesis; pathogenic;

KW immunological response; vaccination; surface disinfectant;

KW personal hygiene application; food preservative; GlmM;

KW phosphoglucosamine-mutase; epitope.

XX

OS Staphylococcus aureus.

XX

PN WO2003025007-A2.

XX

PD 27-MAR-2003.

XX

PF 20-SEP-2002; 2002WO-CA001428.

XX

PR 21-SEP-2001; 2001US-0323992P.

PR 21-SEP-2001; 2001US-0324152P.

PR 25-SEP-2001; 2001US-0324692P.

PR 26-OCT-2001; 2001US-0339924P.

PR 29-OCT-2001; 2001US-0350973P.

PR 30-OCT-2001; 2001US-0340924P.

PR 27-NOV-2001; 2001US-0333666P.

PR 18-DEC-2001; 2001US-0341732P.

PR 18-DEC-2001; 2001US-0341776P.

PR 19-DEC-2001; 2001US-0341949P.

XX

PA (AFFI-) AFFINIUM PHARM INC.

XX

PI Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B;

PI Domagala M, Houston S, Kanagarajah D, Nethery K, Ng I, Mansoury K;  
PI Mcdonald M, Pinder B, Viola C, Wrezel O;  
XX  
DR WPI; 2003-468119/44.

XX  
PT Novel crystallized recombinant polypeptides from Staphylococcus aureus,  
PT Streptococcus pneumoniae and Escherichia coli and which are involved in  
PT membrane biosynthesis, useful as targets for pathogenic bacteria.

XX  
PS Disclosure; SEQ ID NO 88; 325pp; English.

XX  
CC This invention relates to the structural and functional characterisation  
CC of microbial polypeptides from Staphylococcus aureus (S. aureus),  
CC Streptococcus pneumoniae (S. pneumoniae) and Escherichia coli (E. coli)  
CC that provide novel antimicrobial targets. Specifically, it refers to  
CC polypeptides that are involved in membrane biosynthesis, which play a  
CC critical role in the life cycle and viability of their pathogenic species  
CC of origin, and hence provide valuable drug targets. Furthermore, the  
CC invention describes modified version of these proteins that facilitate  
CC characterisation by labelling with isotopic or heavy atoms, and also  
CC fusion proteins. These proteins provide structural and functional  
CC information to aid the discovery of therapeutic molecules to treat  
CC disorders associated with a particular pathogenic species. As such, they  
CC are useful for inducing an immunological response in an individual and as  
CC an antigen for vaccination purposes. The polypeptides are also useful for  
CC developing antimicrobial agents for use as surface disinfectants,  
CC personal hygiene applications and as food preservatives or in treating  
CC food products to eliminate potential pathogens. This peptide sequence is  
CC a predicted epitopic sequence of the S. aureus GlmM protein of the  
CC invention.

XX  
SQ Sequence 10 AA;

Query Match 33.7%; Score 30; DB 7; Length 10;  
Best Local Similarity 55.6%; Pred. No. 3.9e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLLQVMME 13  
:|::||:|  
Db 2 EPLVRVMVE 10

RESULT 36  
AAM96749

ID AAM96749 standard; peptide; 14 AA.

XX

AC AAM96749;

XX

DT 24-JAN-2002 (first entry)

XX

DE Human peptide #24 encoded by a SNP oligonucleotide.

XX

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;

KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200147944-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US035498.  
 XX  
 PR 28-DEC-1999; 99US-0173419P.  
 PR 27-DEC-2000; 2000US-00173419.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shimkets RA, Leach M;  
 XX  
 DR WPI; 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.  
 XX  
 PS Disclosure; Page 3673; 4143pp; English.  
 XX  
 CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms  
 XX  
 SQ Sequence 14 AA;

Query Match 33.7%; Score 30; DB 4; Length 14;  
 Best Local Similarity 46.2%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 PQPLLQVMMEPQG 16  
 |::| :|:: ||  
 Db 1 PRPLRRVVLFYQG 13

RESULT 37  
 AAM47320

ID AAM47320 standard; peptide; 15 AA.

XX

AC AAM47320;

XX

DT 22-FEB-2002 (first entry)

XX

DE Human zinc finger structural domain 52 N-terminal peptide.

XX

KW Human; zinc finger structural domain 52; cancer; nosohaemia;

KW immunological disease; HIV infection; inflammation; gene therapy.

XX

OS Homo sapiens.

XX

PN CN1306987-A.

XX

PD 08-AUG-2001.

XX

PF 28-JAN-2000; 2000CN-00111572.

XX

PR 28-JAN-2000; 2000CN-00111572.

XX

PA (BODA-) BODAO GENE TECH CO LTD SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-026871/04.

XX

PT Polypeptide-zinc finger structural domain 52 and polynucleotide for

PT coding said polypeptide.

XX

PS Example 6; Page 18(Disclosure); 35pp; Chinese.

XX

CC The present invention provides the protein and coding sequences of human

CC zinc finger structural domain 52. The sequences can be used in the

CC treatment of cancer, nosohaemia, HIV infection, immunological diseases

CC and inflammation. The present sequence is the N-terminus of the protein

CC of the invention

XX

SQ Sequence 15 AA;

Query Match 33.7%; Score 30; DB 5; Length 15;

Best Local Similarity 42.9%; Pred. No. 6e+02;

Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14

:||| || | |

Db 1 METPTPLPPVPASP 14

RESULT 38

ABR30169

ID ABR30169 standard; peptide; 15 AA.

XX

AC ABR30169;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #3013.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 470; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 15 AA;

Query Match 33.7%; Score 30; DB 6; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 6e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 PQPLLQVMMEP 14  
 | | : | : | |  
 Db 5 PPPIKQCSLEP 15

RESULT 39  
 ABR30262

ID ABR30262 standard; peptide; 15 AA.  
 XX  
 AC ABR30262;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 74P3B3 HLA peptide #3106.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 471; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 15 AA;  
  
 Query Match 33.7%; Score 30; DB 6; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 6e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
 Qy 4 PQPLLQVMMEP 14

Db                    | | : | : ||  
                      4 PPPIKQCSLEP 14

RESULT 40

ABR30274

ID    ABR30274 standard; peptide; 15 AA.

XX

AC    ABR30274;

XX

DT    19-MAY-2003    (first entry)

XX

DE    Human cancer-related protein 74P3B3 HLA peptide #3118.

XX

KW    Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW    human leukocyte antigen.

XX

OS    Homo sapiens.

XX

PN    WO200283921-A2.

XX

PD    24-OCT-2002.

XX

PF    10-APR-2002; 2002WO-US011654.

XX

PR    10-APR-2001; 2001US-0282739P.

PR    10-APR-2001; 2001US-0283112P.

PR    25-APR-2001; 2001US-0286630P.

XX

PA    (AGEN-) AGENSYS INC.

XX

PI    Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI    Morrison K, Morrison RK, Raitano AB;

XX

DR    WPI; 2003-075555/07.

XX

PT    New composition comprising a substance that modulates the structure of  
PT    proteins and polynucleotides, useful for therapeutic, prognostic and  
PT    diagnostic reagents for eliciting cellular or humoral immune response in  
PT    cancer patients.

XX

PS    Claim 13; Page 472; 1021pp; English.

XX

CC    The present invention relates to novel human cancer-related genes and  
CC    proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC    proteins are useful for eliciting a humoral or cellular immune response.  
CC    The genes are useful as probes and primers for the amplification and/or  
CC    detection of genes, mRNAs or their fragments, as reagents for the  
CC    diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC    directing the expression of the protein, as tools for modulating or  
CC    inhibiting the expression of genes and/or translation of transcripts, and  
CC    as therapeutic agents. The proteins and peptides are useful as  
CC    therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC    sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC    from the invention

XX

SQ    Sequence 15 AA;

Query Match 33.7%; Score 30; DB 6; Length 15;  
Best Local Similarity 45.5%; Pred. No. 6e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 PQPLLQVMMEP 14  
| |: | :||  
Db 5 PPPIKQCSLEP 15

RESULT 41

ABR30229

ID ABR30229 standard; peptide; 15 AA.

XX

AC ABR30229;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #3073.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 471; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 15 AA;

Query Match 33.7%; Score 30; DB 6; Length 15;  
Best Local Similarity 45.5%; Pred. No. 6e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 PQPLLQVMMEP 14  
| |: | :||  
Db 4 PPPIKQCSLEP 14

RESULT 42

ABR30154

ID ABR30154 standard; peptide; 15 AA.

XX

AC ABR30154;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #2998.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 469; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 15 AA;

Query Match 33.7%; Score 30; DB 6; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 6e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 PQPLLQVMMEP 14  
 | |: | :||  
 Db 2 PPPIKQCSLEP 12

# RESULT 43

ABR31758

ID ABR31758 standard; peptide; 15 AA.

XX

AC ABR31758;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 109P1D4 HLA peptide #1530.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in

PT cancer patients.  
 XX  
 PS Claim 13; Page 498; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 15 AA;

Query Match 33.7%; Score 30; DB 6; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 6e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TPQPLLQVMME 13  
 :||| |: |  
 Db 5 SPQPAFQIQPE 15

#### RESULT 44

ABR30297

ID ABR30297 standard; peptide; 15 AA.

XX

AC ABR30297;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #3141.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 472; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 15 AA;

Query Match 33.7%; Score 30; DB 6; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 6e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 PQPLLQVMMEP 14  
 | | : | : ||  
 Db 5 PPPIKQCSLEP 15

#### RESULT 45

AAAY65560

ID AAY65560 standard; peptide; 16 AA.

XX

AC AAY65560;

XX

DT 01-FEB-2000 (first entry)

XX

DE Oestrogen receptor alpha ERE binding peptide 15E.

XX

KW Oestrogen receptor; estrogen; estradiol; oestrogen response element; ERE;  
 KW binding; biological activity; fingerprint; molecular braille;  
 KW cellular braille; modulation; tamoxifen; breast cancer; ovarian cancer;  
 KW menopause; osteoporosis; selective oestrogen receptor modulator;  
 KW identification; characterisation; classification.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9954728-A2.

XX

PD 28-OCT-1999.

XX

PF 26-MAR-1999; 99WO-US006664.

XX

PR 23-APR-1998; 98US-0082756P.

PR 09-SEP-1998; 98US-0099656P.

PR 08-JAN-1999; 99US-0115345P.

XX

PA (NOVA-) NOVALON PHARM CORP.

XX

PI Paige LA, Hamilton PT, Fowlkes DM, Buehrer B, Barnett T;

PI Mcdonnell DP, Christensen DJ;

XX

DR WPI; 2000-013281/01.

XX

PT Methods for identifying new receptor modulators, especially estrogen

PT modulators to treat tamoxifen refractory breast cancer.

XX

PS Example 2.2; Page 161; 219pp; English.

XX

CC The present invention describes a method for predicting the biological  
CC activity of new receptor modulating compounds (I) using novel oligomeric  
CC peptides (biokeys) which have differential abilities to bind to 2  
CC different receptor conformations. The method is used to identify new  
CC drugs that are physiological or pharmacological agonists/antagonists and  
CC that target various receptors, which are involved in certain disease  
CC conditions. The system may be used as a primary screening tool to  
CC identify hits, to classify lead compounds from a drug screen to,  
CC characterise selective oestrogen receptor modulators (SERMs) in terms of  
CC agonist and antagonist function and to predict possible clinical effects  
CC of SERMs such as tissue and receptor specificity. The method can also be  
CC applied to the fractionation of mixtures of SERMs to determine which  
CC components are producing agonistic and antagonistic activity. The method  
CC may be used with other receptors (e.g. progesterone, androgen,  
CC glucocorticoid, thyroid, vitamin D, beta-adrenergic, dopamine and  
CC epidermal growth factor, to identify, characterise and classify  
CC modulators of receptor activity. Peptides comprising a LXXLL motif may be  
CC used to modulate the oestrogen receptor in treating e.g. breast and  
CC ovarian cancer and ameliorating the effects of menopause, including  
CC osteoporosis. AAY65439 to AAY65652 represent oestrogen receptor,  
CC estradiol receptor and oestrogen response element binding peptides given  
CC in the exemplification of the present invention. AAZ35740 to AAZ35745  
CC represent oligonucleotides used in the exemplification of the present  
CC invention

XX

SQ Sequence 16 AA;

Query Match 33.7%; Score 30; DB 3; Length 16;

Best Local Similarity 45.5%; Pred. No. 6.4e+02;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 PLLQVMMEPQG 16

||| :: ||

Db 5 PLLMALLAPPG 15

RESULT 46

AAU86297

ID AAU86297 standard; peptide; 16 AA.

XX  
AC AAU86297;  
XX  
DT 21-MAY-2002 (first entry)  
XX  
DE Oestrogen receptor alpha binding peptide 15E.  
XX  
KW Oestrogen receptor; breast cancer; combinatorial peptide library;  
KW receptor modulating compound.  
XX  
OS Synthetic.  
XX  
PN WO200204956-A2.  
XX  
PD 17-JAN-2002.  
XX  
PF 11-JUL-2001; 2001WO-US021867.  
XX  
PR 12-JUL-2000; 2000US-00614865.  
PR 21-MAY-2001; 2001US-00860688.  
XX  
PA (KARO-) KARO BIO USA INC.  
XX  
PI Fowlkes DM, Barnett TR, Buehrer B;  
XX  
DR WPI; 2002-154969/20.  
XX  
PT Identifying receptor-binding peptides comprises screening combinatorial  
PT peptide library presented in form of cells each of which coexpress one  
PT peptide member and receptor with signal producing system for reporting  
PT binding.  
XX  
PS Disclosure; Page 144; 175pp; English.  
XX  
CC The invention relates to identifying a binding peptide which binds a  
CC receptor and which is a member of a combinatorial library of peptides,  
CC comprising screening a combinatorial peptide library presented in the  
CC form of cells which coexpress the receptor or its ligand-binding receptor  
CC moiety and one member of the library, together with a signal producing  
CC system for reporting binding of the peptide to the receptor. Also  
CC included is a method for predicting the receptor-modulating activity of a  
CC compound which modulates the biological activity of a receptor comprising  
CC (a) identifying peptides which bind the receptor by the method above, (b)  
CC using a number of the peptides to predict the receptor- modulating  
CC activity of a compound by (i) providing a panel of identified peptides,  
CC where the members differ in their ability to bind to the receptor  
CC depending on reference conformations the receptor is in, where the effect  
CC of a number of reference substances known to modulate the biological  
CC activity of the receptor on the binding of each member of the panel is  
CC known and is characterised as a reference fingerprint for each reference  
CC substance, (ii) screening a test substance of unknown activity relative  
CC to the receptor to determine its effect on the binding of each member of  
CC the panel to the receptor, thereby obtaining a test fingerprint for the  
CC test substance, (iii) comparing the test fingerprint to the reference  
CC fingerprints and (iv) predicting the biological activity of the test  
CC substance based on the assumption that its biological activity will be  
CC similar to that of reference substances with similar fingerprints. The

CC method is useful for identifying a binding peptide which binds a  
 CC vertebrate, mammalian, preferably human receptor, an intracellular,  
 CC nuclear, oestrogen or androgen receptor. The identified peptides which  
 CC bind to the receptor are useful for predicting the receptor-modulating  
 CC activity of a compound (e.g. ant/agonists). The receptor-binding library  
 CC members are useful in the prediction of the ability of small organic  
 CC molecules, suitable for pharmaceutical use (e.g. in the case of oestrogen  
 CC receptors, for breast cancer treatment), to interact with the receptor.  
 CC The analyte-binding molecules can also be used for in vivo imaging. The  
 CC method has several advantages over whole animal-based assay systems in  
 CC that the same technology can be applied to a variety of different  
 CC receptors, the system can be used for high throughput screening and  
 CC compound characterisation, and gives very distinct patterns for agonists  
 CC and antagonists of receptor activity using very much less protein. The  
 CC present sequence is an oestrogen receptor binding peptide from a  
 CC combinatorial peptide library

XX

SQ Sequence 16 AA;

Query Match 33.7%; Score 30; DB 5; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 6.4e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 PLLQVMMEPQG 16  
 ||| :: ||  
 Db 5 PLLMALLAPPG 15

# RESULT 47

AAU01845

ID AAU01845 standard; peptide; 17 AA.

XX

AC AAU01845;

XX

DT 07-SEP-2001 (first entry)

XX

DE Wheat peptide antagonist for A-gliadin 57-73 QE65 #7.

XX

KW Wheat; A-gliadin; 57-75 QE65; coeliac disease; gluten intolerance;

KW T-cell binding; antagonist; transglutaminase; transgenic plant.

XX

OS Triticum aestivum.

XX

PN WO200125793-A2.

XX

PD 12-APR-2001.

XX

PF 02-OCT-2000; 2000WO-GB003760.

XX

PR 01-OCT-1999; 99GB-00023306.

XX

PA (ISIS-) ISIS INNOVATION LTD.

XX

PI Anderson RP, Hill AVS, Jewell DP;

XX

DR WPI; 2001-300179/31.

XX

PT Diagnosing coeliac disease or susceptibility to the disease in an  
PT individual, by detecting in vitro or in vivo T cells which bind  
PT immunodominant T cell epitope obtained from naturally occurring homolog  
PT of gliadin.

XX

PS Example 11; Page 58; 107pp; English.

XX

CC The sequence represents a gliadin peptide corresponding to A-gliadin 57-  
CC 73 which is naturally polymorphic in that region and is antagonistic to A  
CC -gliadin 57-73 QE65 interferon gamma ELISpot (not defined) response. The  
CC peptides of the invention are used to test mammalian (preferably human)  
CC susceptibility to coeliac disease (gluten intolerance). The peptides are  
CC contacted with a blood sample and T cell recognition measured, a positive  
CC T-cell recognition indicating a susceptibility to coeliac disease. The  
CC peptides are useful for inducing tolerance in an individual and  
CC antagonists to the peptides are useful for treating or preventing coeliac  
CC disease in an individual and for producing an antibody specific to them  
CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15  
CC amino acids in length) whose wild-type sequence can be modified by  
CC transglutaminase to a sequence that comprises the epitope, but which has  
CC been modified in such a way that it does not contain sequence which can  
CC be modified by transglutaminase to a sequence that comprise the epitope  
CC is useful for decreasing the ability of gliadin protein to cause Coeliac  
CC disease. Nucleic acids encoding proteins antagonistic to the T-cell  
CC binding of the epitopes are useful for obtaining a transgenic plant cell  
CC or seed and for the production of a protein. The resultant crop plant is  
CC useful for obtaining a product of a wheat plant, especially grain, which  
CC is optionally processed into flour or another grain product. Food  
CC comprising the antagonistic protein is useful instead of a wild-type  
CC gliadin

XX

SQ Sequence 17 AA;

Query Match 33.7%; Score 30; DB 4; Length 17;  
Best Local Similarity 50.0%; Pred. No. 6.8e+02;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 PQPLLQVMMEPQ 15  
||| | : ||  
Db 3 PQPFLPELPYPQ 14

#### RESULT 48

AAU01825

ID AAU01825 standard; peptide; 17 AA.

XX

AC AAU01825;

XX

DT 07-SEP-2001 (first entry)

XX

DE Wheat Gliadin peptide M.

XX

KW Wheat; A-gliadin; peptide M; coeliac disease; gluten intolerance;

KW T-cell binding; antagonist; transglutaminase; transgenic plant.

XX

OS Triticum aestivum.

XX

PN WO200125793-A2.

XX

PD 12-APR-2001.

XX

PF 02-OCT-2000; 2000WO-GB003760.

XX

PR 01-OCT-1999; 99GB-00023306.

XX

PA (ISIS-) ISIS INNOVATION LTD.

XX

PI Anderson RP, Hill AVS, Jewell DP;

XX

DR WPI; 2001-300179/31.

XX

PT Diagnosing coeliac disease or susceptibility to the disease in an  
PT individual, by detecting in vitro or in vivo T cells which bind  
PT immunodominant T cell epitope obtained from naturally occurring homolog  
PT of gliadin.

XX

PS Example 8; Fig 14; 107pp; English.

XX

CC The sequence represents wheat Gliadin peptide M, corresponding to A-  
CC gliadin 57-73 and containing a natural polymorphism. The peptides of the  
CC invention are used to test mammalian (preferably human) susceptibility to  
CC coeliac disease (gluten intolerance). The peptides are contacted with a  
CC blood sample and T cell recognition measured, a positive T-cell  
CC recognition indicating a susceptibility to coeliac disease. The peptides  
CC are useful for inducing tolerance in an individual and antagonists to the  
CC peptides are useful for treating or preventing coeliac disease in an  
CC individual and for producing an antibody specific to them or a wild-type  
CC sequence. A mutant gliadin protein (or its fragment of 15 amino acids in  
CC length) whose wild-type sequence can be modified by transglutaminase to a  
CC sequence that comprises the epitope, but which has been modified in such  
CC a way that it does not contain sequence which can be modified by  
CC transglutaminase to a sequence that comprise the epitope is useful for  
CC decreasing the ability of gliadin protein to cause Coeliac disease.  
CC Nucleic acids encoding proteins antagonistic to the T-cell binding of the  
CC epitopes are useful for obtaining a transgenic plant cell or seed and for  
CC the production of a protein. The resultant crop plant is useful for  
CC obtaining a product of a wheat plant, especially grain, which is  
CC optionally processed into flour or another grain product. Food comprising  
CC the antagonistic protein is useful instead of a wild-type gliadin

XX

SQ Sequence 17 AA;

Query Match 33.7%; Score 30; DB 4; Length 17;

Best Local Similarity 50.0%; Pred. No. 6.8e+02;

Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 PQPLLQVMMEPQ 15

||| | : ||

Db 3 PQPFLPQLPYPQ 14

RESULT 49

ABP73085

ID ABP73085 standard; peptide; 8 AA.

XX  
 AC ABP73085;  
 XX  
 DT 17-JUN-2003 (first entry)  
 XX  
 DE Amino acid sequence of an epitope derived from KSHV.  
 XX  
 KW Epitope; KSHV; CD8 T cell; vaccine; dendritic cell; T lymphocyte.  
 XX  
 OS Synthetic.  
 OS Kaposi's sarcoma herpesvirus.  
 XX  
 PN WO2003014154-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 05-AUG-2002; 2002WO-GB003594.  
 XX  
 PR 03-AUG-2001; 2001GB-00019038.  
 XX  
 PA (UNLO ) UNIV COLLEGE LONDON.  
 XX  
 PI Boshoff C;  
 XX  
 DR WPI; 2003-289909/28.  
 XX  
 PT New polypeptides and expression vectors with an epitope sequence  
 PT recognized by a CD8 T cell, useful in the manufacture of a vaccine for  
 PT the prophylactic and/or therapeutic treatment of Kaposi's sarcoma  
 PT herpesvirus infection.  
 XX  
 PS Claim 2; Page 49; 58pp; English.  
 XX  
 CC The present sequence represents an epitope, of a formula given in the  
 CC specification. The epitope is derived from Kaposi's sarcoma herpesvirus  
 CC (KSHV), and is recognised by CD8 T cells. Polypeptides comprising the  
 CC epitope are useful for producing a vaccine against KSHV. They are also  
 CC useful for stimulating dendritic cells or T lymphocytes ex vivo  
 XX  
 SQ Sequence 8 AA;

Query Match 32.6%; Score 29; DB 6; Length 8;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PQPLLQ 9  
 |||:|  
 Db 2 PQPVLQ 7

RESULT 50  
 ABB08361  
 ID ABB08361 standard; protein; 9 AA.  
 XX  
 AC ABB08361;  
 XX  
 DT 07-MAY-2002 (first entry)

XX  
DE Synthetic epitope 1 of human cancer antigen eIF3.  
XX  
KW Human; melanoma antigen eukaryotic initiation factor 3; eIF3;  
KW ovarian cancer; MHC; cytostatic; immunomodulator; immune effector cell;  
KW anti-cancer; vaccine.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 1  
FT /note= "HLA-2 binding residue"  
FT Domain 2  
FT /note= "HLA-2 binding residue"  
FT Domain 3. .8  
FT /note= "T-cell receptor (TCR) binding domain"  
FT Domain 9  
FT /note= "HLA-2 binding residue"  
XX  
PN WO200192307-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 30-MAY-2001; 2001WO-US017456.  
XX  
PR 31-MAY-2000; 2000US-0209391P.  
PR 17-AUG-2000; 2000US-0226258P.  
PR 20-DEC-2000; 2000US-0257008P.  
XX  
PA (GENZ ) GENZYME CORP.  
XX  
PI Nicolette CA;  
XX  
DR WPI; 2002-139606/18.  
XX  
PT New therapeutic compounds useful against human ovarian cancer, for  
PT modulating immune response in a subject, and for generating antibodies  
PT that specifically recognize and bind to these molecules.  
XX  
PS Claim 29; Page 59; 68pp; English.  
XX  
CC The invention relates to novel therapeutic compounds, that are designed  
CC to enhance binding to MHC molecules and to enhance immunoregulatory  
CC properties relative to their natural counterparts. The activity of the  
CC compounds of the invention may be described as cytostatic and  
CC immunomodulatory. The compounds are useful against human ovarian cancer,  
CC for modulating immune response in a subject, and for generating  
CC antibodies that specifically recognize and bind to these molecules.  
CC Compositions comprising the compounds are useful as components of anti-  
CC cancer vaccines and to expand immune effector cells that are specific for  
CC cells characterised by expression of antigen EIF3 (melanoma antigen  
CC eukaryotic initiation factor). The peptides or polypeptides conjugated to  
CC a detectable agent may be used in diagnostic procedures, such as in the  
CC detection and purification of antibodies, and as immunogens for  
CC production of antibodies. The polynucleotides can be used as primers for  
CC detecting genes or gene transcripts expressed in APC to confirm  
CC transduction of the polynucleotides into host cells. The current sequence

CC represents synthetic epitope 1 of human cancer antigen eIF3

XX

SQ Sequence 9 AA;

Query Match 32.6%; Score 29; DB 5; Length 9;

Best Local Similarity 71.4%; Pred. No. 1.4e+06;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LQVMMEP 14

||::|||

Db 2 LQLLMEP 8

Search completed: July 4, 2004, 04:40:35

Job time : 43.8358 secs

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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:37:26 ; Search time 10.6567 Seconds  
 (without alignments)  
 82.356 Million cell updates/sec

Title: US-09-641-802-2  
 Perfect score: 89  
 Sequence: 1 LQTPQPLLQVMMEPQGD 17

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121837

Minimum DB seq length: 7  
 Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	89	100.0	17	4	US-09-641-803-2	Sequence 2, Appli
2	33	37.1	15	4	US-09-641-803-34	Sequence 34, Appl
3	32	36.0	8	5	PCT-US91-05177-19	Sequence 19, Appl
4	31	34.8	13	2	US-08-162-081B-5	Sequence 5, Appli
5	31	34.8	13	2	US-08-780-872-5	Sequence 5, Appli
6	31	34.8	13	3	US-09-085-957-5	Sequence 5, Appli
7	31	34.8	15	1	US-08-477-877B-30	Sequence 30, Appl
8	31	34.8	15	2	US-08-472-281A-30	Sequence 30, Appl
9	31	34.8	15	2	US-08-477-989B-30	Sequence 30, Appl
10	29	32.6	18	2	US-09-017-205-35	Sequence 35, Appl
11	28	31.5	7	1	US-08-594-447-74	Sequence 74, Appl

12	28	31.5	7	1	US-08-541-964-73	Sequence 73, Appl
13	28	31.5	7	2	US-08-665-647-88	Sequence 88, Appl
14	28	31.5	10	3	US-08-981-392-53	Sequence 53, Appl
15	28	31.5	15	2	US-08-553-257A-21	Sequence 21, Appl
16	28	31.5	15	4	US-09-441-992-21	Sequence 21, Appl
17	28	31.5	16	3	US-08-602-999A-195	Sequence 195, App
18	28	31.5	16	4	US-09-500-124-195	Sequence 195, App
19	27	30.3	15	3	US-08-646-265A-125	Sequence 125, App
20	27	30.3	15	4	US-09-947-372A-27	Sequence 27, Appl
21	27	30.3	16	3	US-08-837-226-2	Sequence 2, Appli
22	27	30.3	16	4	US-09-537-226-2	Sequence 2, Appli
23	26.5	29.8	18	4	US-09-829-855-240	Sequence 240, App
24	26	29.2	8	4	US-08-475-955-182	Sequence 182, App
25	26	29.2	8	4	US-08-475-955-185	Sequence 185, App
26	26	29.2	9	3	US-08-159-339A-1062	Sequence 1062, Ap
27	26	29.2	9	4	US-08-737-109-5	Sequence 5, Appli
28	26	29.2	9	6	5204326-100	Patent No. 5204326
29	26	29.2	10	3	US-08-159-339A-971	Sequence 971, App
30	26	29.2	10	3	US-08-159-339A-1070	Sequence 1070, Ap
31	26	29.2	13	3	US-09-023-173-9	Sequence 9, Appli
32	26	29.2	13	3	US-09-023-339-7	Sequence 7, Appli
33	26	29.2	14	4	US-08-855-744-2	Sequence 2, Appli
34	26	29.2	14	6	5204326-36	Patent No. 5204326
35	26	29.2	14	6	5204326-95	Patent No. 5204326
36	26	29.2	15	3	US-08-096-044C-14	Sequence 14, Appl
37	26	29.2	15	6	5204326-37	Patent No. 5204326
38	26	29.2	15	6	5204326-40	Patent No. 5204326
39	26	29.2	15	6	5204326-71	Patent No. 5204326
40	26	29.2	15	6	5204326-74	Patent No. 5204326
41	26	29.2	16	1	US-07-700-526-8	Sequence 8, Appli
42	26	29.2	16	3	US-08-096-044C-13	Sequence 13, Appl
43	26	29.2	16	3	US-08-096-044C-15	Sequence 15, Appl
44	26	29.2	16	5	PCT-US92-03132-8	Sequence 8, Appli
45	26	29.2	16	6	5204326-96	Patent No. 5204326
46	26	29.2	17	2	US-08-675-921B-7	Sequence 7, Appli
47	26	29.2	17	6	5204326-97	Patent No. 5204326
48	26	29.2	18	6	5204326-38	Patent No. 5204326
49	26	29.2	18	6	5204326-41	Patent No. 5204326
50	26	29.2	18	6	5204326-98	Patent No. 5204326
51	26	29.2	18	6	5204326-101	Patent No. 5204326
52	25	28.1	7	1	US-08-594-447-75	Sequence 75, Appl
53	25	28.1	7	1	US-08-541-964-74	Sequence 74, Appl
54	25	28.1	7	2	US-08-665-647-89	Sequence 89, Appl
55	25	28.1	7	3	US-09-467-423-80	Sequence 80, Appl
56	25	28.1	7	3	US-09-467-423-94	Sequence 94, Appl
57	25	28.1	7	3	US-09-467-423-166	Sequence 166, App
58	25	28.1	7	3	US-09-467-423-180	Sequence 180, App
59	25	28.1	7	4	US-09-467-426-80	Sequence 80, Appl
60	25	28.1	7	4	US-09-467-426-94	Sequence 94, Appl
61	25	28.1	7	4	US-09-467-426-166	Sequence 166, App
62	25	28.1	7	4	US-09-467-426-180	Sequence 180, App
63	25	28.1	8	3	US-09-467-423-65	Sequence 65, Appl
64	25	28.1	8	3	US-09-467-423-79	Sequence 79, Appl
65	25	28.1	8	3	US-09-467-423-93	Sequence 93, Appl
66	25	28.1	8	3	US-09-467-423-151	Sequence 151, App
67	25	28.1	8	3	US-09-467-423-165	Sequence 165, App
68	25	28.1	8	3	US-09-467-423-179	Sequence 179, App

69	25	28.1	8	4	US-09-467-426-65	Sequence 65, Appl
70	25	28.1	8	4	US-09-467-426-79	Sequence 79, Appl
71	25	28.1	8	4	US-09-467-426-93	Sequence 93, Appl
72	25	28.1	8	4	US-09-467-426-151	Sequence 151, App
73	25	28.1	8	4	US-09-467-426-165	Sequence 165, App
74	25	28.1	8	4	US-09-467-426-179	Sequence 179, App
75	25	28.1	9	1	US-08-421-702A-19	Sequence 19, Appl
76	25	28.1	9	1	US-08-421-702A-113	Sequence 113, App
77	25	28.1	9	1	US-08-421-702A-116	Sequence 116, App
78	25	28.1	9	1	US-08-303-052A-19	Sequence 19, Appl
79	25	28.1	9	1	US-08-303-052A-55	Sequence 55, Appl
80	25	28.1	9	1	US-08-303-052A-113	Sequence 113, App
81	25	28.1	9	1	US-08-421-696A-19	Sequence 19, Appl
82	25	28.1	9	1	US-08-421-696A-113	Sequence 113, App
83	25	28.1	9	1	US-08-421-696A-116	Sequence 116, App
84	25	28.1	9	1	US-08-421-697A-19	Sequence 19, Appl
85	25	28.1	9	1	US-08-421-697A-113	Sequence 113, App
86	25	28.1	9	1	US-08-421-697A-116	Sequence 116, App
87	25	28.1	9	1	US-08-421-698A-19	Sequence 19, Appl
88	25	28.1	9	1	US-08-421-698A-113	Sequence 113, App
89	25	28.1	9	1	US-08-421-698A-116	Sequence 116, App
90	25	28.1	9	2	US-08-421-695A-19	Sequence 19, Appl
91	25	28.1	9	2	US-08-421-695A-55	Sequence 55, Appl
92	25	28.1	9	2	US-08-421-695A-114	Sequence 114, App
93	25	28.1	9	2	US-08-421-695A-128	Sequence 128, App
94	25	28.1	9	3	US-09-467-423-51	Sequence 51, Appl
95	25	28.1	9	3	US-09-467-423-64	Sequence 64, Appl
96	25	28.1	9	3	US-09-467-423-78	Sequence 78, Appl
97	25	28.1	9	3	US-09-467-423-92	Sequence 92, Appl
98	25	28.1	9	3	US-09-467-423-137	Sequence 137, App
99	25	28.1	9	3	US-09-467-423-150	Sequence 150, App
100	25	28.1	9	3	US-09-467-423-164	Sequence 164, App

# ALIGNMENTS

```

RESULT 1
US-09-641-803-2
; Sequence 2, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT

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; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-2

Query Match 100.0%; Score 89; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQGD 17  
| | | | | | | | | | | | | | | | |  
Db 1 LQTPQPLLQVMMEPQGD 17

RESULT 2

US-09-641-803-34

; Sequence 34, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-34

Query Match 37.1%; Score 33; DB 4; Length 15;  
Best Local Similarity 53.8%; Pred. No. 41;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14  
| | | | | : | |  
Db 3 QPPQPLPPTVMFP 15

RESULT 3

PCT-US91-05177-19

; Sequence 19, Application PC/TUS9105177  
; GENERAL INFORMATION:  
; APPLICANT: Berkner, Kathy L  
; TITLE OF INVENTION: GAMMA-CARBOXYLASE AND METHODS OF USE  
; NUMBER OF SEQUENCES: 21

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Seed and Berry
;   STREET:  6300 Columbia Center, 701 Fifth Avenue
;   CITY:  Seattle
;   STATE:  WA
;   COUNTRY:  USA
;   ZIP:  98104-7092
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US91/05177
;   FILING DATE:  19910722
;   CLASSIFICATION:  800
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/557,220
;   FILING DATE:  23-JUL-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Maki, David J
;   REGISTRATION NUMBER:  31,392
;   REFERENCE/DOCKET NUMBER:  990008.544PC
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  206-622-4900
;   TELEFAX:  206-682-6031
;   INFORMATION FOR SEQ ID NO:  19:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  8 amino acids
;   TYPE:  AMINO ACID
;   TOPOLOGY:  linear
;   FRAGMENT TYPE:  internal
PCT-US91-05177-19

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```

Query Match          36.0%;  Score 32;  DB 5;  Length 8;
Best Local Similarity 100.0%;  Pred. No. 3e+05;
Matches      6;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      3 TPQPLL 8
        |||||
Db      1 TPQPLL 6

```

#### RESULT 4

US-08-162-081B-5

```

; Sequence 5, Application US/08162081B
; Patent No. 5824492

```

#### GENERAL INFORMATION:

```

;   APPLICANT:  Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
;   APPLICANT:  Bala; Waterfield, Michael Derek; Parker, Peter
;   APPLICANT:  Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
;   APPLICANT:  Stefano; Gout, Ivan Tarasovitch
;   TITLE OF INVENTION:  POLYPEPTIDES HAVING KINASE ACTIVITY,
;   TITLE OF INVENTION:  THEIR PREPARATION AND USE
;   NUMBER OF SEQUENCES:  50
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Felte & Lynch

```

```

; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,081B
; FILING DATE: February 7, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-162-081B-5

```

```

Query Match          34.8%; Score 31; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 73;
Matches      5; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

```

```

Qy      4 PQPLLQVMME 13
        | || :||:
Db      4 PDPLYEVMLK 13

```

# RESULT 5

US-08-780-872-5

```

; Sequence 5, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York

```

```

; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-780-872-5

```

```

Query Match          34.8%; Score 31; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 73;
Matches      5; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

```

```

Qy      4 PQPLLQVMME 13
        | || :||:
Db      4 PDPLYEVMLK 13

```

# RESULT 6

US-09-085-957-5

```

; Sequence 5, Application US/09085957
; Patent No. 6274327
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York

```

```

; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,957
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/780,872
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-085-957-5

```

```

Query Match          34.8%; Score 31; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 73;
Matches    5; Conservative    3; Mismatches    2; Indels    0; Gaps    0;

```

```

Qy      4 PQPLLQVMME 13
        | || :||:
Db      4 PDPLYEVMLK 13

```

# RESULT 7

US-08-477-877B-30

```

; Sequence 30, Application US/08477877B
; Patent No. 5730979

```

## GENERAL INFORMATION:

```

; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-
Cell Activati
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road

```

```

;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07068
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,877B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,009
;      FILING DATE:  29-MAR-1995
;      APPLICATION NUMBER:  08/119,032
;      FILING DATE:  09-SEP-1993
;      APPLICATION NUMBER:  08/027,008
;      FILING DATE:  05-MAR-1993
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  61750-146
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;      INFORMATION FOR SEQ ID NO:  30:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  polypeptide
US-08-477-877B-30

```

```

Query Match          34.8%;  Score 31;  DB 1;  Length 15;
Best Local Similarity  71.4%;  Pred. No. 85;
Matches      5;  Conservative    2;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      2 QTPQPLL 8
        |:||||:
Db      8 QSPQPLI 14

```

```

RESULT 8
US-08-472-281A-30
; Sequence 30, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT:  Bazin, Herv
; APPLICANT:  Latinne, Dominique
; TITLE OF INVENTION:  LO-CD2a Antibody and Uses Thereof for Inhibiting T-
Cell Activati
; NUMBER OF SEQUENCES:  96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,

```

```

;   ADDRESSEE:  Cecchi, Stewart & Olstein
;   STREET:    6 Becker Farm Road
;   CITY:      Roseland
;   STATE:     New Jersey
;   COUNTRY:   U.S.A.
;   ZIP:       07068
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch diskette
;   COMPUTER:   IBM PS/2
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE:   WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/472,281A
;   FILING DATE:  07-JUN-1995
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/407,009
;   FILING DATE: 29-MAR-1995
;   APPLICATION NUMBER: 08/119,032
;   FILING DATE: 09-SEP-1993
;   APPLICATION NUMBER: 08/027,008
;   FILING DATE: 05-MAR-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME:       Olstein, Elliot M.
;   REGISTRATION NUMBER: 24,025
;   REFERENCE/DOCKET NUMBER: 61750-142
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  201-994-1700
;   TELEFAX:    201-994-1744
;   INFORMATION FOR SEQ ID NO: 30:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:     15 amino acids
;   TYPE:        amino acid
;   STRANDEDNESS:
;   TOPOLOGY:    linear
;   MOLECULE TYPE: polypeptide
US-08-472-281A-30

```

```

Query Match          34.8%;  Score 31;  DB 2;  Length 15;
Best Local Similarity 71.4%;  Pred. No. 85;
Matches      5;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      2 QTPQPLL 8
        |:||||:
Db      8 QSPQPLI 14

```

```

RESULT 9
US-08-477-989B-30
; Sequence 30, Application US/08477989B
; Patent No. 5951983
; GENERAL INFORMATION:
;   APPLICANT:  Bazin, Herv
;   APPLICANT:  Latinne, Dominique
;   APPLICANT:  Kaplan, Ruth
;   APPLICANT:  Kieber-Emmons, Thomas
;   APPLICANT:  Postema, Christina E.

```

```

; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,989B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-477-989B-30

```

```

Query Match          34.8%; Score 31; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 85;
Matches      5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 QTPQPLL 8
        |:||||:
Db      8 QSPQPLI 14

```

```

RESULT 10
US-09-017-205-35

```

```

; Sequence 35, Application US/09017205
; Patent No. 5965357
; GENERAL INFORMATION:
;   APPLICANT: Marsden, Howard S
;   TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
;   TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
;   NUMBER OF SEQUENCES: 86
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Nixon & Vanderhye PC
;     STREET: 8th Floor, 1100 No. 5965357th Glebe Road
;     CITY: Arlington
;     STATE: Virginia
;     COUNTRY: USA
;     ZIP: 22201-4714
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/017,205
;     FILING DATE: 02-FEB-1998
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Mitchard, Leonard C
;     REGISTRATION NUMBER: 29,009
;     REFERENCE/DOCKET NUMBER: 604-436
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (703)816-4000
;     TELEFAX: (703)816-4100
;   INFORMATION FOR SEQ ID NO: 35:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 18 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide from HSV-2 glycoprotein G
;     FRAGMENT TYPE: internal
US-09-017-205-35

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```

Query Match          32.6%; Score 29; DB 2; Length 18;
Best Local Similarity 37.5%; Pred. No. 2.1e+02;
Matches      6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

```

Qy      2 QTPQPLLQVMMEPQGD 17
        :|| |:  | | |
Db      1 KTPLPVSATAMAPSVD 16

```

```

RESULT 11
US-08-594-447-74
; Sequence 74, Application US/08594447
; Patent No. 5776716
; GENERAL INFORMATION:
;   APPLICANT: Ron, Dorit
;   APPLICANT: Napolitano, Eugene W.
;   APPLICANT: Voronova, Anna F.
;   TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH

```

```

; TITLE OF INVENTION: BLOCKTHE INTERACTION OF FYN WITH PKC-THETA, AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,447
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /label= PRK1-3
US-08-594-447-74

```

```

Query Match          31.5%; Score 28; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      12 MEPQG 16
        |||||
Db      1 MEPQG 5

```

```

RESULT 12
US-08-541-964-73
; Sequence 73, Application US/08541964
; Patent No. 5783405
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; APPLICANT: Kauvar, Lawrence M.

```

```

; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS
; TITLE OF INVENTION: OF SIGNAL TRANSDUCTION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,964
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /label= PRK1-3
US-08-541-964-73

```

```

Query Match          31.5%; Score 28; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      12 MEPQG 16
        |||||
Db      1 MEPQG 5

```

```

RESULT 13
US-08-665-647-88
; Sequence 88, Application US/08665647
; Patent No. 5935803
; GENERAL INFORMATION:
; APPLICANT: Dasquez, Nicki J.
; APPLICANT: Ron, Dorit

```

```

; APPLICANT: Voronova, Anna F.
; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS
; TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,647
; FILING DATE: 18-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /label= PRK1-3
US-08-665-647-88

```

```

Query Match          31.5%; Score 28; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      12 MEPQG 16
        |||||
Db      1 MEPQG 5

```

```

RESULT 14
US-08-981-392-53
; Sequence 53, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David

```

```

; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-981-392-53

```

```

Query Match          31.5%; Score 28; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches      5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      4 PQPLLQVMME 13
        ||||:: |
Db      1 PQPLVRTEQE 10

```

# RESULT 15

US-08-553-257A-21

; Sequence 21, Application US/08553257A

; Patent No. 5994083

; GENERAL INFORMATION:

; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA

; APPLICANT: MOLECOLARE P. ANGELETTI S.p.A.

; APPLICANT: FELICI, Franco

```

; APPLICANT: LUZZAGO, Alessandra
; APPLICANT: NICOSIA, Alfredo
; APPLICANT: MONACI, Paolo
; APPLICANT: CORTESE, Riccardo
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
; TITLE OF INVENTION: OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
; TITLE OF INVENTION: DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,257A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IT94/00054
; FILING DATE: 05-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: RM93A000301
; FILING DATE: 11-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: recombinant protein
; HYPOTHETICAL: yes
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; LIBRARY: of recombinant peptides on phage
; CLONE: phagic
; FEATURE:
; NAME/KEY: polypeptide
; IDENTIFICATION METHOD: selection with specific antibodies
US-08-553-257A-21

```

```

Query Match          31.5%; Score 28; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches      8; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

```

Qy 2 QTPQPLLQVMMEPQGD 17  
| | | | |  
Db 4 QVPQSRL----EPWGD 15

RESULT 16

US-09-441-992-21

; Sequence 21, Application US/09441992

; Patent No. 6541210

; GENERAL INFORMATION:

; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA

; MOLECOLARE P. ANGELETTI S.p.A.

; FELICI, Franco

; LUZZAGO, Alessandra

; NICOSIA, Alfredo

; MONACI, Paolo

; CORTESE, Riccardo

; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS

; OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR

; DIAGNOSTIC REAGENTS THEREBY OBTAINABLE

; NUMBER OF SEQUENCES: 68

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Browdy and Neimark

; STREET: 419 Seventh Street N.W. Ste. 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/441,992

; FILING DATE: 18-No. 6541210-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/553,257

; FILING DATE: <Unknown>

; APPLICATION NUMBER: RM93A000301

; FILING DATE: 11-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Browdy, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: FELICI=1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 628-5197

; TELEFAX: (202) 737-3528

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: recombinant protein

```

;      HYPOTHETICAL: yes
;      FRAGMENT TYPE: internal
;      IMMEDIATE SOURCE:
;          LIBRARY: of recombinant peptides on phage
;          CLONE: phagic
;              (ix)  FEATURE
;              (A)  NAME: polypeptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-441-992-21

```

```

Query Match          31.5%;  Score 28;  DB 4;  Length 15;
Best Local Similarity 50.0%;  Pred. No. 2.5e+02;
Matches      8;  Conservative    0;  Mismatches    4;  Indels      4;  Gaps      1;

```

```

Qy      2 QTPQPLLQVMMEPQGD 17
        | || |   || ||
Db      4 QVPQSRL----EPWGD 15

```

# RESULT 17

US-08-602-999A-195

; Sequence 195, Application US/08602999A

; Patent No. 6184205

## ; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

## ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A

; FILING DATE: 16-FEB-1996

; CLASSIFICATION: 435

## ; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

## ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 195:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-195

Query Match 31.5%; Score 28; DB 3; Length 16;  
Best Local Similarity 41.7%; Pred. No. 2.7e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TPQPLLQVMMEP 14  
||:| : | |  
Db 4 TPRPAVPQRMNP 15

RESULT 18

US-09-500-124-195

; Sequence 195, Application US/09500124  
; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 195:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-195

Query Match 31.5%; Score 28; DB 4; Length 16;  
Best Local Similarity 41.7%; Pred. No. 2.7e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TPQPLLQVMMEP 14  
| | : | |  
Db 4 TPRPAVPQRMNP 15

RESULT 19

US-08-646-265A-125

; Sequence 125, Application US/08646265A  
; Patent No. 6214973

; GENERAL INFORMATION:

; APPLICANT: OHTOMO, Toshihiko  
; APPLICANT: SATO, Koh  
; APPLICANT: TSUCHIYA, Masayuki  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/646,265A  
; FILING DATE: 09-SEP-1996  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/JP94/01763  
; FILING DATE: 19-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 5-291078  
; FILING DATE: 19-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/184

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 125:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-646-265A-125

Query Match 30.3%; Score 27; DB 3; Length 15;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8  
|:|:|:  
Db 8 QSPKPLI 14

RESULT 20  
US-09-947-372A-27  
; Sequence 27, Application US/09947372A  
; Patent No. 6613557  
; GENERAL INFORMATION:  
; APPLICANT: FRAZER, IAN  
; APPLICANT: ZHOU, JIAN  
; TITLE OF INVENTION: PAPILLOMAVIRUS VACCINE  
; FILE REFERENCE: 065064/0137  
; CURRENT APPLICATION NUMBER: US/09/947,372A  
; CURRENT FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: 08/185,928  
; PRIOR FILING DATE: 1994-01-19  
; PRIOR APPLICATION NUMBER: PCT/AU92/02184  
; PRIOR FILING DATE: 1992-07-20  
; PRIOR APPLICATION NUMBER: AU PK7322  
; PRIOR FILING DATE: 1991-07-19  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-09-947-372A-27

Query Match 30.3%; Score 27; DB 4; Length 15;  
Best Local Similarity 40.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 8 LQVMMEPQGD 17  
::: || ||  
Db 1 IKMVSEPYGD 10

RESULT 21  
US-08-837-226-2

```

; Sequence 2, Application US/08837226
; Patent No. 6043216
; GENERAL INFORMATION:
;   APPLICANT: Toback, F. Gary
;   APPLICANT: Lieske, John C.
;   TITLE OF INVENTION: METHODS AND COMPOSITION FOR DETECTING
;   TITLE OF INVENTION: AND TREATING KIDNEY DISEASES ASSOCIATED WITH ADHESION
OF
;   TITLE OF INVENTION: CRYSTALS TO KIDNEY CELLS
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
;     STREET: NBC Tower - Suite 3600, 455 N. Cityfront
;     STREET: Plaza Drive
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: USA
;     ZIP: 60611-5599
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/837,226
;     FILING DATE: 08-APR-1997
;     CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/389,005
;     FILING DATE: 15-FEB-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Martin, Alice O.
;     REGISTRATION NUMBER: 35,601
;     REFERENCE/DOCKET NUMBER: 7814/24
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 312-321-4200
;     TELEFAX: 312-321-4299
;   INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 16 amino acids
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-08-837-226-2

```

```

Query Match          30.3%; Score 27; DB 3; Length 16;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches      5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      4 PQPLLQ 9
        |||||
Db     10 PQPLYQ 15

```

```

RESULT 22
US-09-537-226-2

```

```
; Sequence 2, Application US/09537226
; Patent No. 6482934
; GENERAL INFORMATION:
; APPLICANT: TOBACK, F. GARY
; APPLICANT: LIESKE, JOHN C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
; TITLE OF INVENTION: KIDNEY DISEASES ASSOCIATED WITH ADHESION OF CRYSTALS TO
; TITLE OF INVENTION: KIDNEY CELLS
; FILE REFERENCE: 21459/90606
; CURRENT APPLICATION NUMBER: US/09/537,226
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/389,005
; PRIOR FILING DATE: 1995-02-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-537-226-2
```

```
Query Match          30.3%; Score 27; DB 4; Length 16;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches      5; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy          4 PQPLLQ 9
             |||| |
Db          10 PQPLYQ 15
```

#### RESULT 23

US-09-829-855-240

```
; Sequence 240, Application US/09829855
; Patent No. 6613520
; GENERAL INFORMATION:
; APPLICANT: Matthew, Ashby N.
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of
Populations
; FILE REFERENCE: ASHBY-1
; CURRENT APPLICATION NUMBER: US/09/829,855
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/196063
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/196258
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured Acidobacterium Sub.Div-2
US-09-829-855-240
```

Query Match 29.8%; Score 26.5; DB 4; Length 18;  
Best Local Similarity 58.3%; Pred. No. 5.3e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 5 QPLLQVMMEPQG 16  
|| | |: |||  
Db 3 QP-LHVVATPQG 13

RESULT 24

US-08-475-955-182

; Sequence 182, Application US/08475955

; Patent No. 6641813

; GENERAL INFORMATION:

; APPLICANT: Harley, John

; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF

; TITLE OF INVENTION: AUTOANTIBODIES

; NUMBER OF SEQUENCES: 218

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street

; CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/475,955

; FILING DATE: June 7, 1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/867,819

; FILING DATE: April 13, 1992

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/648,205

; FILING DATE: January 31, 1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/472,947

; FILING DATE: January 31, 1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404)-873-8794

; TELEFAX: (404)-873-8795

; INFORMATION FOR SEQ ID NO: 182:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-475-955-182

Query Match 29.2%; Score 26; DB 4; Length 8;  
Best Local Similarity 62.5%; Pred. No. 3e+05;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 QVMMEPQG 16  
| :| |||  
Db 1 QQVMTPQG 8

RESULT 25

US-08-475-955-185

; Sequence 185, Application US/08475955  
; Patent No. 6641813  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
; TITLE OF INVENTION: AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 218  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,955  
; FILING DATE: June 7, 1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/867,819  
; FILING DATE: April 13, 1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/648,205  
; FILING DATE: January 31, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/472,947  
; FILING DATE: January 31, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-873-8794  
; TELEFAX: (404)-873-8795  
; INFORMATION FOR SEQ ID NO: 185:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-475-955-185

Query Match 29.2%; Score 26; DB 4; Length 8;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 MEPQGD 17  
| |||:  
Db 1 MTPQGB 6

RESULT 26

US-08-159-339A-1062

; Sequence 1062, Application US/08159339A  
; Patent No. 6037135

; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; TITLE OF INVENTION: Uses  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1062:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-159-339A-1062

Query Match 29.2%; Score 26; DB 3; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPQGD 17  
:||||  
Db 1 QPQGD 5

RESULT 27

US-08-737-109-5

; Sequence 5, Application US/08737109  
; Patent No. 6455688  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, Antoni Ryszard  
; APPLICANT: ELBOROUGH, Kieran Michael  
; APPLICANT: BRIGHT, Simon William Jonathan  
; APPLICANT: FENTEM, Philip Anthony  
; TITLE OF INVENTION: Plant Gene Specifying Acetyl Coenzyme A  
; TITLE OF INVENTION: Carboxylase and Transformed Plants Containing Same  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,109  
; FILING DATE: 21-OCT-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB94/00846  
; FILING DATE: 02-MAY-1994  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO

; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; ORGANISM: Avena sativa  
US-08-737-109-5

Query Match 29.2%; Score 26; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MMEPQG 16  
::||||  
Db 2 VLEPQG 7

RESULT 28

5204326-100

;Patent No. 5204326

; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO  
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
;METABOLISM IMPROVING AGENT

; NUMBER OF SEQUENCES: 147

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/493,359

; FILING DATE: 14-MAR-1990

;SEQ ID NO:100:

; LENGTH: 9

5204326-100

Query Match 29.2%; Score 26; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
|||||  
Db 3 LQTPQ 7

RESULT 29

US-08-159-339A-971

; Sequence 971, Application US/08159339A

; Patent No. 6037135

; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Sette, Alessandro

; APPLICANT: Celis, Esteban

; TITLE OF INVENTION: HLA Binding peptides and Their

; TITLE OF INVENTION: Uses

; NUMBER OF SEQUENCES: 1254

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

```

;      ZIP: 94111-3834
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: DOS
;      SOFTWARE: FastSEQ for Windows Version 2.0
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/159,339A
;      FILING DATE: 29-NOV-1993
;      CLASSIFICATION: 424
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US 07/926,666
;      FILING DATE: 07-AUG-1992
;      APPLICATION NUMBER: US 08/027,746
;      FILING DATE: 05-MAR-1993
;      APPLICATION NUMBER: US 08/103,396
;      FILING DATE: 06-AUG-1993
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Weber, Ellen Lauver
;      REGISTRATION NUMBER: 32,762
;      REFERENCE/DOCKET NUMBER: 018623-005030US
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 576-0200
;      TELEFAX: (415) 576-0300
;      TELEX:
;      INFORMATION FOR SEQ ID NO: 971:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 10 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
US-08-159-339A-971

```

```

Query Match          29.2%; Score 26; DB 3; Length 10;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches      4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      13 EPQGD 17
        :||||
Db      5 QPQGD 9

```

# RESULT 30

US-08-159-339A-1070

; Sequence 1070, Application US/08159339A

; Patent No. 6037135

; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Sette, Alessandro

; APPLICANT: Celis, Esteban

; TITLE OF INVENTION: HLA Binding peptides and Their

; TITLE OF INVENTION: Uses

; NUMBER OF SEQUENCES: 1254

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

```

; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1070:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1070

```

```

Query Match          29.2%; Score 26; DB 3; Length 10;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches      4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      13 EPQGD 17
        :||||
Db      1 QPQGD 5

```

```

RESULT 31
US-09-023-173-9
; Sequence 9, Application US/09023173
; Patent No. 6066781
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of Mature Proteins
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 23

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,173
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,168
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R
; REGISTRATION NUMBER: P42995
; REFERENCE/DOCKET NUMBER: 0665-0007.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: N-terminal amino acid sequence of mature AAT
US-09-023-173-9

```

```

Query Match          29.2%; Score 26; DB 3; Length 13;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches      4; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      13 EPQGD 17
        :||||
Db      2 DPQGD 6

```

```

RESULT 32
US-09-023-339-7
; Sequence 7, Application US/09023339
; Patent No. 6127145
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of `1-Antitrypsin
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,339
; FILING DATE: 13-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,991
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 0665-0003.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: N-terminal sequence of plant-produced mature AAT
US-09-023-339-7

```

```

Query Match          29.2%; Score 26; DB 3; Length 13;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches      4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      13 EPQGD 17
        :||||
Db      2 DPQGD 6

```

# RESULT 33

US-08-855-744-2

```

; Sequence 2, Application US/08855744
; Patent No. 6685930
; GENERAL INFORMATION:
; APPLICANT: Chang, Tse Wen
; TITLE OF INVENTION: METHODS AND SUBSTANCES FOR RECRUITING
; TITLE OF INVENTION: THERAPEUTIC AGENTS TO SOLID TISSUES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas

```

```

; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Hi Density Diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS, Version 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,744
; FILING DATE: 08-May-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,649
; FILING DATE:
; APPLICATION NUMBER: US/07/675,654
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TNX91-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-664-2288
; TELEFAX: 713-664-8914
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
US-08-855-744-2

```

```

Query Match          29.2%; Score 26; DB 4; Length 14;
Best Local Similarity 62.5%; Pred. No. 4.8e+02;
Matches      5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      3 TPQPLLQV 10
        || | :||
Db      4 TPSPGIQV 11

```

```

RESULT 34
5204326-36
;Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
;SEQ ID NO:36:
; LENGTH: 14
5204326-36

```

```

Query Match          29.2%; Score 26; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;

```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
 |||||

Db 2 LQTPQ 6

RESULT 35

5204326-95

; Patent No. 5204326

; APPLICANT: FUJII, SETSURO; YAMAMOTO, YOSHIHITO; SHIMIZU, FUMIO  
 ; INAI, MASATOSHI; KINOSHITA, NAOSUMI; NAKAMURA, SHIZUO; HIROHASHI,  
 ; MITSURU; SAKAMOTO, TAKASHI; TSUTSUMI, KAZUHIKO; SHIRASAKA, TETSUHIKO  
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
 ; METABOLISM IMPROVING AGENT

; NUMBER OF SEQUENCES: 147

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/493,359

; FILING DATE: 14-MAR-1990

; SEQ ID NO: 95:

; LENGTH: 14

5204326-95

Query Match 29.2%; Score 26; DB 6; Length 14;

Best Local Similarity 100.0%; Pred. No. 4.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
 |||||

Db 2 LQTPQ 6

RESULT 36

US-08-096-044C-14

; Sequence 14, Application US/08096044C

; Patent No. 6153192

; GENERAL INFORMATION:

; APPLICANT: Kopetzki, Erhard, Klein, Christian  
 ; TITLE OF INVENTION: PEPTIDES WITH CHARACTERISTIC  
 ; TITLE OF INVENTION: ANTIGENIC DETERMINANTS FOR  
 ; TITLE OF INVENTION: 1-MICROGLOBULIN  
 ; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte & Lynch

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/096,044C

; FILING DATE: July 22, 1993

```

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 40 24 919
; FILING DATE: August 6, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Bauer, John A.
; REGISTRATION NUMBER: 32,554
; REFERENCE/DOCKET NUMBER: HUBR 1000.1-PFF/JAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-096-044C-14

```

```

Query Match          29.2%; Score 26; DB 3; Length 15;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches      4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 QTPQPLL 8
        | | : | : |
Db      6 QEPEPIL 12

```

```

RESULT 37
5204326-37
;Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
;SEQ ID NO:37:
; LENGTH: 15
5204326-37

```

```

Query Match          29.2%; Score 26; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 LQTPQ 5
        | | | |
Db      3 LQTPQ 7

```

```

RESULT 38
5204326-40
;Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO

```

;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
;METABOLISM IMPROVING AGENT  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
;SEQ ID NO:40:  
; LENGTH: 15  
5204326-40

Query Match 29.2%; Score 26; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
| | | | |  
Db 3 LQTPQ 7

RESULT 39  
5204326-71

;Patent No. 5204326  
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO  
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
;METABOLISM IMPROVING AGENT  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
;SEQ ID NO:71:  
; LENGTH: 15  
5204326-71

Query Match 29.2%; Score 26; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
| | | | |  
Db 3 LQTPQ 7

RESULT 40  
5204326-74

;Patent No. 5204326  
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO  
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
;METABOLISM IMPROVING AGENT  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359

; FILING DATE: 14-MAR-1990  
;SEQ ID NO:74:  
; LENGTH: 15  
5204326-74

Query Match 29.2%; Score 26; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
|||||  
Db 3 LQTPQ 7

RESULT 41

US-07-700-526-8

; Sequence 8, Application US/07700526  
; Patent No. 5166133  
; GENERAL INFORMATION:  
; APPLICANT: Houston, L. L.  
; APPLICANT: Liu, David Y.  
; APPLICANT: Kaymakcalan, Zehra  
; TITLE OF INVENTION: Method for Inhibiting Adhesion of White  
; TITLE OF INVENTION: Blood Cells to Endothelial Cells  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cetus Corporation  
; STREET: 1400 Fifty-Third Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/700,526  
; FILING DATE: 19910816  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McGarrigle Jr., Philip L.  
; REGISTRATION NUMBER: 31,395  
; REFERENCE/DOCKET NUMBER: 2600.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 420-3217  
; TELEFAX: (415) 658-5239  
; TELEX: 4992659  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-700-526-8

Query Match 29.2%; Score 26; DB 1; Length 16;  
Best Local Similarity 57.1%; Pred. No. 5.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8  
| | : | : |  
Db 8 QEPEPIL 14

RESULT 42

US-08-096-044C-13

; Sequence 13, Application US/08096044C

; Patent No. 6153192

; GENERAL INFORMATION:

; APPLICANT: Kopetzki, Erhard, Klein, Christian  
; TITLE OF INVENTION: PEPTIDES WITH CHARACTERISTIC  
; TITLE OF INVENTION: ANTIGENIC DETERMINANTS FOR  
; TITLE OF INVENTION: 1-MICROGLOBULIN  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felte & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/096,044C  
; FILING DATE: July 22, 1993  
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE 40 24 919  
; FILING DATE: August 6, 1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Bauer, John A.  
; REGISTRATION NUMBER: 32,554  
; REFERENCE/DOCKET NUMBER: HUBR 1000.1-PFF/JAB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-096-044C-13

Query Match 29.2%; Score 26; DB 3; Length 16;  
Best Local Similarity 57.1%; Pred. No. 5.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8  
| | : | : |  
Db 7 QEPEPIL 13

RESULT 43

US-08-096-044C-15

; Sequence 15, Application US/08096044C  
; Patent No. 6153192  
; GENERAL INFORMATION:  
; APPLICANT: Kopetzki, Erhard, Klein, Christian  
; TITLE OF INVENTION: PEPTIDES WITH CHARACTERISTIC  
; TITLE OF INVENTION: ANTIGENIC DETERMINANTS FOR  
; TITLE OF INVENTION: 1-MICROGLOBULIN  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felte & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/096,044C  
; FILING DATE: July 22, 1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 40 24 919  
; FILING DATE: August 6, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bauer, John A.  
; REGISTRATION NUMBER: 32,554  
; REFERENCE/DOCKET NUMBER: HUBR 1000.1-PFF/JAB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-096-044C-15

Query Match 29.2%; Score 26; DB 3; Length 16;  
Best Local Similarity 57.1%; Pred. No. 5.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8  
| | : | : |  
Db 7 QEPEPIL 13

RESULT 44

PCT-US92-03132-8

; Sequence 8, Application PC/TUS9203132

; GENERAL INFORMATION:

; APPLICANT: Houston, L. L.

; APPLICANT: Liu, David Y.

; APPLICANT: Kaymakcalan, Zehra

; TITLE OF INVENTION: Method for Inhibiting Adhesion of White

; TITLE OF INVENTION: Blood Cells to Endothelial Cells

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cetus Corporation

; STREET: 1400 Fifty-Third Street

; CITY: Emeryville

; STATE: CA

; COUNTRY: USA

; ZIP: 94608

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/03132

; FILING DATE: 19920416

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/700,526

; FILING DATE: 14-MAY-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: McGarrigle Jr., Philip L.

; REGISTRATION NUMBER: 31,395

; REFERENCE/DOCKET NUMBER: 2600.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 420-3217

; TELEFAX: (415) 658-5239

; TELEX: 4992659

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US92-03132-8

Query Match 29.2%; Score 26; DB 5; Length 16;

Best Local Similarity 57.1%; Pred. No. 5.6e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8

| | : | : |

Db 8 QEPEPIL 14

RESULT 45

5204326-96

;Patent No. 5204326

; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO  
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO

; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
;METABOLISM IMPROVING AGENT

; NUMBER OF SEQUENCES: 147

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/493,359

; FILING DATE: 14-MAR-1990

;SEQ ID NO:96:

; LENGTH: 16

5204326-96

Query Match 29.2%; Score 26; DB 6; Length 16;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5

||||

Db 4 LQTPQ 8

RESULT 46

US-08-675-921B-7

; Sequence 7, Application US/08675921B

; Patent No. 5863728

; GENERAL INFORMATION:

; APPLICANT: John Siu-Cheong Ho, John T. Loh, Melvin

; APPLICANT: Schindler and John L. Wang

; TITLE OF INVENTION: DNA Encoding Carbohydrate

; TITLE OF INVENTION: Binding Protein and Biological

; TITLE OF INVENTION: Materials Derived Therefrom

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ian C. McLeod

; STREET: 2190 Commons Parkway

; CITY: Okemos

; STATE: Michigan

; COUNTRY: USA

; ZIP: 48864

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette 5.25 inch, 360

; MEDIUM TYPE: Kb storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS (version 3.3)

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/675,921B

; FILING DATE: 06/05/96

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

```

; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-265
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: No. 5863728e
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Peptide
; HYPOTHETICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE: N/A
; ORIGINAL SOURCE: N/A
; ORGANISM: N/A
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE:
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: deduced partial amino acid
; NAME/KEY: sequence of BJ38 DNA
; LOCATION: N/A
; IDENTIFICATION METHOD: N/A
; OTHER INFORMATION: N/A
; PUBLICATION INFORMATION: N/A
US-08-675-921B-7

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Query Match          29.2%; Score 26; DB 2; Length 17;
Best Local Similarity 33.3%; Pred. No. 6e+02;
Matches      5; Conservative      5; Mismatches      5; Indels      0; Gaps      0;

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Qy      3 TPQPLLQVMMEPQGD 17
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Db      1 TPQEVVFLVTDGVGD 15

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RESULT 47
5204326-97
;Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
;METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147

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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
;SEQ ID NO:97:  
; LENGTH: 17  
5204326-97

Query Match 29.2%; Score 26; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
|||||  
Db 5 LQTPQ 9

RESULT 48  
5204326-38

;Patent No. 5204326  
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO  
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
;METABOLISM IMPROVING AGENT  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
;SEQ ID NO:38:  
; LENGTH: 18  
5204326-38

Query Match 29.2%; Score 26; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
|||||  
Db 6 LQTPQ 10

RESULT 49  
5204326-41

;Patent No. 5204326  
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO  
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
;METABOLISM IMPROVING AGENT  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
;SEQ ID NO:41:  
; LENGTH: 18  
5204326-41

Query Match 29.2%; Score 26; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
|||||  
Db 6 LQTPQ 10

RESULT 50  
5204326-98  
;Patent No. 5204326  
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO  
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,  
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
;METABOLISM IMPROVING AGENT  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
;SEQ ID NO:98:  
; LENGTH: 18  
5204326-98

Query Match 29.2%; Score 26; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
|||||  
Db 6 LQTPQ 10

Search completed: July 4, 2004, 04:48:45  
Job time : 12.6567 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:35:16 ; Search time 13.0672 Seconds  
(without alignments)  
125.142 Million cell updates/sec

Title: US-09-641-802-2  
Perfect score: 89  
Sequence: 1 LQTPQPLLQVMMEPQGD 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2898

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	25	28.1	14	2	C44823	synaptosomal-assoc
2	25	28.1	18	2	A35704	cytochrome P450 ol
3	25	28.1	18	2	F49215	urease (EC 3.5.1.5
4	24	27.0	10	2	A61218	alpha-gliadin 4Ha
5	24	27.0	15	2	A61391	alpha-1-antitrypsi
6	23	25.8	11	2	PC2330	cycloinulooligosac
7	23	25.8	12	2	S70344	amine oxidase (cop
8	23	25.8	15	2	E56819	PS I complex subun
9	23	25.8	16	2	PS0210	28K protein 4209 -
10	23	25.8	16	2	A46236	transforming prote
11	23	25.8	18	2	I59649	human leukocyte an
12	21	23.6	10	2	B61218	alpha-gliadin 6Ha
13	21	23.6	12	2	PH1567	cerebrin 28 - huma

14	21	23.6	14	2	PN0147	omega-gliadine 1 a
15	21	23.6	14	2	PH1566	cerebrin 30 - huma
16	21	23.6	15	2	A40634	orf19 3' of eryK -
17	21	23.6	15	2	A42413	Ig heavy chain V r
18	21	23.6	17	2	PC1318	large granule L6 c
19	21	23.6	18	2	PN0149	beta-Gliadine 13 -
20	21	23.6	18	2	S78767	ribosomal protein
21	20	22.5	10	2	PX0030	triacylglycerol li
22	20	22.5	10	2	PQ0788	NADH2 dehydrogenas
23	20	22.5	13	2	D39690	neural cell adhesi
24	20	22.5	14	2	PC7075	guanylate cyclase
25	20	22.5	15	2	PA0021	protein QA300016 -
26	20	22.5	15	2	PN0148	omega-gliadine 3 -
27	20	22.5	15	2	A41436	alpha-macroglobuli
28	20	22.5	15	2	PL0110	complement factor
29	20	22.5	16	2	S00123	dihydrolipoamide S
30	20	22.5	16	2	D83794	hypothetical prote
31	20	22.5	17	2	S33609	extensin - maize (
32	20	22.5	17	2	B31769	T-cell receptor de
33	20	22.5	18	2	S10452	hypothetical prote
34	20	22.5	18	2	I78841	thrombopoietin rec
35	19	21.3	8	2	S21288	lectin - potato (f
36	19	21.3	9	2	S70345	amine oxidase (cop
37	19	21.3	10	2	D33098	214K exoantigen (v
38	19	21.3	10	2	A61007	hementin (EC 3.4.-
39	19	21.3	11	2	S42587	celF protein - Esc
40	19	21.3	11	2	S21127	precorrin methyltr
41	19	21.3	11	2	PN0044	protein kinase C i
42	19	21.3	12	2	A61309	glycoprotein hormo
43	19	21.3	13	2	S36668	hypothetical prote
44	19	21.3	14	2	I54945	gene C protein - E
45	19	21.3	14	2	A39239	actin 8 - slime mo
46	19	21.3	14	2	S12904	protein kinase (EC
47	19	21.3	15	2	A56891	gamma 1 gliadin -
48	19	21.3	15	2	F44823	synaptosomal-assoc
49	19	21.3	16	2	A24099	crystal protein, 2
50	19	21.3	16	2	PH0763	T-cell receptor be
51	19	21.3	16	2	A45454	ankyrin-binding gl
52	19	21.3	17	2	S41207	F420-non-reducing-
53	19	21.3	17	2	S15064	hypothetical prote
54	19	21.3	17	2	D48138	d(TTAGGG)n-binding
55	19	21.3	18	2	I52614	u-plasminogen acti
56	19	21.3	18	2	S52125	gamma2-gliadin P25
57	19	21.3	18	2	D56049	kidney stone prote
58	18.5	20.8	14	2	S00150	ovostatin - duck (
59	18.5	20.8	15	2	B41436	ovostatin - green
60	18.5	20.8	18	2	A61392	brain-associated s
61	18	20.2	9	2	A60108	exotoxin A - Strep
62	18	20.2	10	2	A61622	vitellogenin, 190k
63	18	20.2	11	2	A34662	Achatina cardio-ex
64	18	20.2	12	2	B44818	extracellular lipa
65	18	20.2	12	2	S67528	napin - rape (frag
66	18	20.2	12	2	S70337	napin small chain
67	18	20.2	12	2	PN0046	ATP synthase D cha
68	18	20.2	12	4	JX0315	aminotransferase c
69	18	20.2	13	2	A44818	extracellular lipa
70	18	20.2	13	2	S09716	2S albumin large c

71	18	20.2	13	2	PH1772	T cell receptor al
72	18	20.2	13	2	B47415	mannose-1-phosphat
73	18	20.2	13	2	B56864	dipeptidyl-peptida
74	18	20.2	14	2	PS0278	ribulose-bisphosph
75	18	20.2	15	2	B39109	hypothetical 1.5K
76	18	20.2	15	2	A57003	hypothetical prote
77	18	20.2	15	2	PA0088	protein QF200051 -
78	18	20.2	15	2	A45103	7 alpha-hydroxy-4-
79	18	20.2	15	2	I78838	flt3 ligand isoform
80	18	20.2	16	2	PH0767	T-cell receptor be
81	18	20.2	16	2	PD0002	inulin fructotrans
82	18	20.2	17	2	A60570	Ig mu heavy chain
83	18	20.2	17	2	A35550	adrenocortical cel
84	18	20.2	17	2	B25348	glycogen(starch) s
85	18	20.2	18	2	S46418	NTL1 protein - cur
86	18	20.2	18	2	S28408	platelet-derived g
87	18	20.2	18	2	I46653	T-cell receptor de
88	18	20.2	18	2	A54195	Na+/K+-exchanging
89	17	19.1	7	2	S71299	ICL2 protein - Par
90	17	19.1	8	2	S53008	citrate synthase -
91	17	19.1	9	2	A41978	calliFMRFamide 1 -
92	17	19.1	9	2	S26508	collagen alpha 2(V
93	17	19.1	9	2	PC7074	translation elonga
94	17	19.1	10	2	S33844	alpha-2-macroglobu
95	17	19.1	10	2	B59272	peptide-N4-(N-acet
96	17	19.1	10	2	S71948	matrix metalloprot
97	17	19.1	10	2	E86128	hypothetical prote
98	17	19.1	11	2	S23306	substance P - Atla
99	17	19.1	11	2	S68637	acetylcholinestera
100	17	19.1	12	2	S10059	tachykinin - Afric

#### ALIGNMENTS

##### RESULT 1

C44823

synaptosomal-associated protein SNAP-25 peptide 8 - rabbit (fragment)

N;Alternate names: superprotein peptide 8

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Jun-1996

C;Accession: C44823

R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.

J. Neurosci. 11, 3412-3421, 1991

A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is identical to SNAP-25, a protein of synaptic terminals.

A;Reference number: A44823; MUID:92044785; PMID:1941090

A;Accession: C44823

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <LOE>

A;Experimental source: visual tissue

A;Note: sequence extracted from NCBI backbone (NCBIP:64253)

C;Keywords: membrane trafficking

Query Match 28.1%; Score 25; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 4.8e+02;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 10 VMMEPQGD 17  
 ||:: ||:  
 Db 3 VMLDEQGE 10

# RESULT 2

A35704  
 cytochrome P450 olf2 - bovine (fragment)  
 N;Contains: oxidoreductase (EC 1.-.-.)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 12-Mar-1999  
 C;Accession: A35704  
 R;Lazard, D.; Tal, N.; Rubinstein, M.; Khen, M.; Lancet, D.; Zupko, K.  
 Biochemistry 29, 7433-7440, 1990  
 A;Title: Identification and biochemical analysis of novel olfactory-specific  
 cytochrome P-450IIA and UDP-glucuronosyl transferase.  
 A;Reference number: A35704; MUID:91027757; PMID:2121272  
 A;Accession: A35704  
 A;Molecule type: protein  
 A;Residues: 1-18 <LAZ>  
 C;Genetics:  
 A;Gene: CYP2A  
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology  
 C;Keywords: electron transfer; heme; monooxygenase; oxidoreductase;  
 transmembrane protein

Query Match 28.1%; Score 25; DB 2; Length 18;  
 Best Local Similarity 46.2%; Pred. No. 6.4e+02;  
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 PQPLLQVMMEPQG 16  
 | | | | |  
 Db 5 PGPQQQAFKELQG 17

# RESULT 3

F49215  
 urease (EC 3.5.1.5) small chain UreA - Helicobacter mustelae (ATCC 43772)  
 (fragment)  
 C;Species: Helicobacter mustelae  
 C;Date: 19-Dec-1993 #sequence\_revision 25-Apr-1997 #text\_change 06-Jan-2003  
 C;Accession: F49215  
 R;Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.  
 Infect. Immun. 60, 5259-5266, 1992  
 A;Title: Purification and characterization of the urease enzymes of Helicobacter  
 species from humans and animals.  
 A;Reference number: A49215; MUID:93084378; PMID:1452359  
 A;Accession: F49215  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-18 <TUR>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:119487)  
 C;Superfamily: urease, fused gamma/beta subunit; urease 11K chain homology;  
 urease 12K chain homology  
 C;Keywords: hydrolase

Query Match 28.1%; Score 25; DB 2; Length 18;  
Best Local Similarity 33.3%; Pred. No. 6.4e+02;  
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TPQPLLQVMMEPQGD 17  
||: | :|: |:  
Db 2 TPKELDKMMLHYAGE 16

RESULT 4

A61218

alpha-gliadin 4Ha - grass (*Haynaldia villosa*) (fragment)

C;Species: *Haynaldia villosa*, *Dasypyrum villosum*

C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Mar-1999

C;Accession: A61218

R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.

Biochem. Genet. 29, 207-211, 1991

A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of *Haynaldia villosa* Schur (syn. *Dasypyrum villosum* L.).

A;Reference number: A61218; MUID:91315394; PMID:1859356

A;Accession: A61218

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <SHE>

C;Keywords: seed; storage protein

Query Match 27.0%; Score 24; DB 2; Length 10;  
Best Local Similarity 55.6%; Pred. No. 4.9e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQ 9  
|: | | ||  
Db 2 LRVFPVQLQ 10

RESULT 5

A61391

alpha-1-antitrypsin homolog - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 17-Mar-1999

C;Accession: A61391

R;Tanaka, N.; Sekiya, S.; Takamizawa, H.; Kato, N.; Moriyama, Y.; Fujimura, S.

Jpn. J. Cancer Res. 82, 693-700, 1991

A;Title: Characterization of a 54 kDa, alpha-1-antitrypsin-like protein isolated from ascitic fluid of an endometrial cancer patient.

A;Reference number: A61391; MUID:91310496; PMID:1906855

A;Accession: A61391

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <TAN>

Query Match 27.0%; Score 24; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 PQGD 17

Db                   | | | |  
                      3 PQGD 6

RESULT 6

PC2330

cycloinulooligosaccharide fructanotransferase (EC 2.4.-.-) - *Bacillus circulans* (MCI-2554) (fragment)

C;Species: *Bacillus circulans*

C;Date: 21-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 07-May-1999

C;Accession: PC2330

R;Kushibe, S.; Mitsui, K.; Yamagishi, M.; Yamada, K.; Morimoto, Y.

Biosci. Biotechnol. Biochem. 59, 31-34, 1995

A;Title: Purification and characterization of cycloinulooligosaccharide fructanotransferase (CFTase) from *Bacillus circulans* MCI-2554.

A;Reference number: PC2330; MUID:95201377; PMID:7765973

A;Accession: PC2330

A;Molecule type: protein

A;Residues: 1-11 <KUS>

C;Comment: This enzyme hydrolyzes beta-(2-1) glycosidic linkages and acts in intermolecular transfructosylation.

C;Keywords: glycosyltransferase; hexosyltransferase

Query Match                   25.8%;   Score 23;   DB 2;   Length 11;  
Best Local Similarity   80.0%;   Pred. No. 8e+02;  
Matches   4;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy                   12 MEPQG 16

| | |

Db                   7 MNPQG 11

RESULT 7

S70344

amine oxidase (copper-containing) (EC 1.4.3.6) I - *Aspergillus niger* (fragments)

C;Species: *Aspergillus niger*

C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998

C;Accession: S70344

R;Frebort, I.; Pec, P.; Luhova, L.; Toyama, H.; Matsushita, K.; Hirota, S.;

Kitagawa, T.; Ueno, T.; Asano, Y.; Kato, Y.; Adachi, O.

Biochim. Biophys. Acta 1295, 59-72, 1996

A;Title: Two amine oxidases from *Aspergillus niger* AKU 3302 contain topa quinone as the cofactor: unusual cofactor link to the glutamyl residue occurs only at one of the enzymes.

A;Reference number: S70344; MUID:96283794; PMID:8679675

A;Accession: S70344

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7;8-12 <FRE>

C;Keywords: oxidoreductase

Query Match                   25.8%;   Score 23;   DB 2;   Length 12;  
Best Local Similarity   57.1%;   Pred. No. 8.8e+02;  
Matches   4;   Conservative   2;   Mismatches   1;   Indels   0;   Gaps   0;

Qy                   10 VMMEPQG 16

|::| |

Db 1 VVIEPYG 7

RESULT 8

E56819

PS I complex subunit 8 - cucumber (fragment)

C;Species: Cucumis sativus (cucumber)

C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996

C;Accession: E56819

R;Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.

Biochim. Biophys. Acta 1059, 141-148, 1991

A;Title: Characterization of genes that encode subunits of cucumber PS I complex by N-terminal sequencing.

A;Reference number: A56819; MUID:91355209; PMID:1883835

A;Accession: E56819

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <IWA>

A;Note: sequence extracted from NCBI backbone (NCBIP:58606)

Query Match 25.8%; Score 23; DB 2; Length 15;  
Best Local Similarity 30.8%; Pred. No. 1.1e+03;  
Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
:| | ||: :  
Db 1 IQADXPTFQVIQD 13

RESULT 9

PS0210

28K protein 4209 - rice (strain Nihonbare) (fragment)

C;Species: Oryza sativa (rice)

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995

C;Accession: PS0210

R;Tsugita, A.; Miyatake, N.

submitted to JIPID, April 1993

A;Reference number: PS0208

A;Accession: PS0210

A;Molecule type: protein

A;Residues: 1-16 <TSA>

A;Experimental source: germ, bran, strain Nihonbare

C;Comment: molecular weight 28K, pI 7.3.

Query Match 25.8%; Score 23; DB 2; Length 16;  
Best Local Similarity 37.5%; Pred. No. 1.2e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 10 VMMEPQGD 17  
:: |::|  
Db 8 IVPNPEGD 15

RESULT 10

A46236

transforming protein myc, form 1 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C;Accession: A46236  
R;Hann, S.R.; Sloan-Brown, K.; Spotts, G.D.  
Genes Dev. 6, 1229-1240, 1992  
A;Title: Translational activation of the non-AUG-initiated c-myc 1 protein at high cell densities due to methionine deprivation.  
A;Reference number: A46236; MUID:92331929; PMID:1628829  
A;Accession: A46236  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-16 <HAN>  
A;Cross-references: GB:X01023  
C;Genetics:  
A;Start codon: CTG  
C;Keywords: alternative initiators

Query Match 25.8%; Score 23; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
|:|  
Db 7 LETPQ 11

RESULT 11

I59649

human leukocyte antigen alpha chain - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C;Accession: I59649

R;Fogdell, A.; Olerup, O.

Tissue Antigens 44, 19-24, 1994

A;Title: The DQA1\*0104 allele is carried by DRB1\*1001- and DRB1\*1401-positive haplotypes in Caucasians, Africans and Orientals.

A;Reference number: I59649; MUID:95064785; PMID:7974465

A;Accession: I59649

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-18 <RES>

A;Cross-references: GB:S75685; NID:g913771; PIDN:AAB32621.1; PID:g913772

C;Genetics:

A;Gene: GDB:HLA-DQA1

A;Cross-references: GDB:120638; OMIM:146880

A;Map position: 6p21.3-6p21.3

Query Match 25.8%; Score 23; DB 2; Length 18;  
Best Local Similarity 55.6%; Pred. No. 1.4e+03;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 LQVMMEPQG 16  
| |||  
Db 5 LTTMSPCG 13

RESULT 12

B61218

alpha-gliadin 6Ha - grass (*Haynaldia villosa*) (fragment)  
 C;Species: *Haynaldia villosa*, *Dasypyrum villosum*  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Mar-1999  
 C;Accession: B61218  
 R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
 Biochem. Genet. 29, 207-211, 1991  
 A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of  
*Haynaldia villosa* Schur (syn. *Dasypyrum villosum* L.).  
 A;Reference number: A61218; MUID:91315394; PMID:1859356  
 A;Accession: B61218  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <SHE>  
 C;Keywords: seed; storage protein

Query Match 23.6%; Score 21; DB 2; Length 10;  
 Best Local Similarity 44.4%; Pred. No. 1.6e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQ 9  
 :: ||||  
 Db 1 VRVPVQLQ 9

#### RESULT 13

PH1567  
 cerebrin 28 - human (fragment)  
 C;Species: *Homo sapiens* (man)  
 C;Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
 C;Accession: PH1567  
 R;Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.  
 J. Neurochem. 61, 533-540, 1993  
 A;Title: Micropurification of two human cerebrospinal fluid proteins by high  
 performance electrophoresis chromatography.  
 A;Reference number: PH1566; MUID:93329419; PMID:8336140  
 A;Accession: PH1567  
 A;Molecule type: protein  
 A;Residues: 1-12 <LEO>

Query Match 23.6%; Score 21; DB 2; Length 12;  
 Best Local Similarity 44.4%; Pred. No. 1.9e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 PLLQVMMEP 14  
 | ||::|  
 Db 2 PPAQVSVQP 10

#### RESULT 14

PN0147  
 omega-gliadine 1 and 2 - *Aegilops longissima* (fragment)  
 C;Species: *Aegilops longissima*  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: PN0147; PN0146  
 R;Odintsova, T.I.; Egorov, T.A.  
 Biokhimiia 55, 509-516, 1990

A;Title: N-Terminal sequences of omega-gliadins of *Aegilops longissima*: On the origin of polyploid wheat genomes.

A;Reference number: PN0146; MUID:90283493; PMID:2354218

A;Accession: PN0147

A;Molecule type: protein

A;Residues: 1-14 <ODI>

A;Experimental source: strain K-202

A;Note: omega-gliadine 2 (amino-terminal fragment)

A;Accession: PN0146

A;Molecule type: protein

A;Residues: 1-9 <OD2>

A;Experimental source: strain K-202

A;Note: omega-gliadine 1 (amino-terminal fragment)

Query Match 23.6%; Score 21; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4  
| | | |  
Db 11 LQTP 14

#### RESULT 15

PH1566

cerebrin 30 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999

C;Accession: PH1566

R;Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.  
J. Neurochem. 61, 533-540, 1993

A;Title: Micropurification of two human cerebrospinal fluid proteins by high performance electrophoresis chromatography.

A;Reference number: PH1566; MUID:93329419; PMID:8336140

A;Accession: PH1566

A;Molecule type: protein

A;Residues: 1-14 <LEO>

Query Match 23.6%; Score 21; DB 2; Length 14;  
Best Local Similarity 44.4%; Pred. No. 2.3e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 PLLQVMMEP 14  
| || ::|  
Db 2 PEAQVSVQP 10

#### RESULT 16

A40634

orf19 3' of eryK - *Saccharopolyspora erythraea* (fragment)

C;Species: *Saccharopolyspora erythraea*

C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Nov-1994

C;Accession: A40634

R;Stassi, D.; Donadio, S.; Staver, M.J.; Katz, L.

J. Bacteriol. 175, 182-189, 1993

A;Title: Identification of a *Saccharopolyspora erythraea* gene required for the final hydroxylation step in erythromycin biosynthesis.

A;Reference number: A40634; MUID:93106953; PMID:8416893  
A;Accession: A40634  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-15 <STA>  
A;Note: sequence extracted from NCBI backbone (NCBIN:121243, NCBIP:121244)

Query Match 23.6%; Score 21; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQP 6  
: ||:|  
Db 7 VSTPRP 12

#### RESULT 17

A42413

Ig heavy chain V region (LBL-copurifying) - rabbit (fragment)  
C;Species: *Oryctolagus cuniculus* (domestic rabbit)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 07-May-1999  
C;Accession: A42413  
R; Bao, Z.; Muschler, J.; Horwitz, A.F.  
J. Biol. Chem. 267, 4974-4980, 1992  
A;Title: LBL, a novel, developmentally regulated, laminin-binding lectin.  
A;Reference number: A42413; MUID:92165867; PMID:1531660  
A;Accession: A42413  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <BAO>  
C;Keywords: heterotetramer; immunoglobulin

Query Match 23.6%; Score 21; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4  
||||  
Db 11 LQTP 14

#### RESULT 18

PC1318

large granule L6 chain - horseshoe crab (*Tachypleus tridentatus*) (fragment)  
C;Species: *Tachypleus tridentatus*  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C;Accession: PC1318  
R; Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwanaga, S.  
J. Biochem. 114, 307-316, 1993  
A;Title: Separation of large and small granules from horseshoe crab (*Tachypleus tridentatus*) hemocytes and characterization of their components.  
A;Reference number: PC1309; MUID:94110249; PMID:8282718  
A;Accession: PC1318  
A;Molecule type: protein  
A;Residues: 1-17 <SHI>  
C;Comment: This protein participates in immobilization of invading microbes.

Query Match 23.6%; Score 21; DB 2; Length 17;  
Best Local Similarity 30.8%; Pred. No. 2.8e+03;  
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14  
| | | : : |  
Db 5 QIPGKLMHITATP 17

RESULT 19

PN0149

beta-Gliadine 13 - Aegilops longissima (fragment)

C;Species: Aegilops longissima

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: PN0149

R;Odintsova, T.I.; Egorov, T.A.

Biokhimiia 55, 509-516, 1990

A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of polyploid wheat genomes.

A;Reference number: PN0146; MUID:90283493; PMID:2354218

A;Accession: PN0149

A;Molecule type: protein

A;Residues: 1-18 <ODI>

A;Experimental source: strain K-202

C;Superfamily: gliadin

Query Match 23.6%; Score 21; DB 2; Length 18;  
Best Local Similarity 44.4%; Pred. No. 3e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQ 9  
: : | | | |  
Db 1 VRVPVPQLQ 9

RESULT 20

S78767

ribosomal protein MRP-S29, mitochondrial - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C;Accession: S78767

R;Graack, H.R.

submitted to the Protein Sequence Database, July 1999

A;Reference number: S78760

A;Accession: S78767

A;Molecule type: protein

A;Residues: 1-18 <GRA>

C;Keywords: mitochondrion

F;1-18/Product: ribosomal protein MRP-S29 (fragment) #status experimental <MAT>

Query Match 23.6%; Score 21; DB 2; Length 18;  
Best Local Similarity 33.3%; Pred. No. 3e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LLQVMMEPQ 15  
: | : | | :  
Db

## RESULT 21

PX0030

triacylglycerol lipase (EC 3.1.1.3) II - yeast (*Geotrichum candidum*) (fragments)C;Species: *Geotrichum candidum*

C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 30-Sep-1993

C;Accession: PX0030

R;Sugihara, A.; Shimada, Y.; Tominaga, Y.

J. Biochem. 107, 426-430, 1990

A;Title: Separation and characterization of two molecular forms of *Geotrichum candidum* lipase.

A;Reference number: PX0030; MUID:90256718; PMID:2341377

A;Accession: PX0030

A;Molecule type: protein

A;Residues: 1-10 &lt;SUG&gt;

C;Comment: Lipase catalyzes the hydrolysis of triacylglycerols. This fungus contains two forms of lipase, lipase I and lipase II.

C;Keywords: carboxylic ester hydrolase

Query Match 22.5%; Score 20; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 2.3e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8

: | : | |

Db 1 EAPRPXL 7

## RESULT 22

PQ0788

NADH2 dehydrogenase (EC 1.6.99.3) 20K chain - fava bean mitochondrion (fragment)

N;Alternate names: complex I 20K chain; NADH-ubiquinone reductase 20K chain

C;Species: mitochondrion *Vicia faba* (fava bean)

C;Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 03-Jun-2002

C;Accession: PQ0788

R;Leterme, S.; Boutry, M.

Plant Physiol. 102, 435-443, 1993

A;Title: Purification and preliminary characterization of mitochondrial complex I (NADH:ubiquinone reductase) from broad bean (*Vicia faba* L.).

A;Reference number: PQ0775; MUID:94151437; PMID:8108509

A;Accession: PQ0788

A;Molecule type: protein

A;Residues: 1-10 &lt;LET&gt;

C;Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the three proton-translocating complexes of the mitochondrial respiratory chain and composed of 35 different subunits ranging from 5K to 75K.

C;Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by a large number of redox groups.

C;Genetics:

A;Genome: mitochondrion

C;Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 22.5%; Score 20; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 2.3e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QPLLQV 10  
| ||||  
Db 5 QVLLQV 10

RESULT 23

D39690

neural cell adhesion molecule, cardiac splice form +,-,-,+ - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999

C;Accession: D39690

R;Reyes, A.A.; Small, S.J.; Akesson, R.

Mol. Cell. Biol. 11, 1654-1661, 1991

A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA are expressed during rat heart development.

A;Reference number: A39690; MUID:91141516; PMID:1996115

A;Accession: D39690

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-13 <REY>

A;Cross-references: GB:M63970

C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin homology

C;Keywords: cardiac muscle; cell adhesion; heart

Query Match 22.5%; Score 20; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 14 PQGD 17  
|||:  
Db 8 PQGE 11

RESULT 24

PC7075

guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000

C;Accession: PC7075

R;Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.;

Watanabe, Y.; Morimasa, T.; Hosokawa, K.; Toda, T.

Electrophoresis 21, 1853-1871, 2000

A;Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of tissue proteins during the course of aging.

A;Reference number: PC7072

A;Accession: PC7075

A;Molecule type: protein

A;Residues: 1-14 <TSU>

A;Experimental source: strain C57BL/6Cr Slc, male; brain, striatum

C;Keywords: brain; phosphorus-oxygen lyase

Query Match 22.5%; Score 20; DB 2; Length 14;  
Best Local Similarity 75.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 14 PQGD 17  
| | | :  
Db 9 PQGE 12

RESULT 25

PA0021

protein QA300016 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997

C;Accession: PA0021

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis.

A;Reference number: PA0001

A;Accession: PA0021

A;Molecule type: protein

A;Residues: 1-15 <KAM>

A;Experimental source: leaf

Query Match 22.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 42.9%; Pred. No. 3.6e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 9 QVMMEPQ 15  
: ::| | |  
Db 5 EXVIEPQ 11

RESULT 26

PN0148

omega-gliadine 3 - Aegilops longissima (fragment)

C;Species: Aegilops longissima

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: PN0148

R;Odintsova, T.I.; Egorov, T.A.

Biokhimiia 55, 509-516, 1990

A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of polyploid wheat genomes.

A;Reference number: PN0146; MUID:90283493; PMID:2354218

A;Accession: PN0148

A;Molecule type: protein

A;Residues: 1-15 <ODI>

A;Experimental source: strain K-202

A;Note: 11-Gln was also found

Query Match 22.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.6e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
| | | |  
Db 11 LXTPQ 15

# RESULT 27

A41436

alpha-macroglobulin - green seaturtle (fragment)

C;Species: *Chelonia mydas* (green seaturtle)

C;Date: 21-Apr-1992 #sequence\_revision 21-Apr-1992 #text\_change 18-Jun-1993

C;Accession: A41436

R;Osada, T.; Sasaki, T.; Ikai, A.

J. Biochem. 103, 212-217, 1988

A;Title: Purification and characterization of alpha-macroglobulin and ovomacroglobulin of the green turtle (*Chelonia mydas japonica*).

A;Reference number: A41436; MUID:88227890; PMID:2453503

A;Accession: A41436

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <OSA>

Query Match 22.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 33.3%; Pred. No. 3.6e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 PQPLLQVMM 12

|::| |::

Db 2 PEPQYMLV 10

# RESULT 28

PL0110

complement factor B1-Bb and B2-Bb - guinea pig (fragment)

C;Species: *Cavia porcellus* (guinea pig)

C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 15-Nov-1996

C;Accession: PL0110

R;Matsushita, M.; Okada, H.

Mol. Immunol. 26, 669-676, 1989

A;Title: Two forms of guinea pig factor B of the alternative complement pathway with different molecular weights.

A;Reference number: A93136; MUID:89384686; PMID:2779589

A;Accession: PL0110

A;Molecule type: protein

A;Residues: 1-15 <MAT>

C;Keywords: complement alternate pathway; glycoprotein

Query Match 22.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 28.6%; Pred. No. 3.6e+03;  
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 10 VMMEPQG 16

:::| |

Db 2 IILDPA 8

# RESULT 29

S00123

dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) - bovine (fragment)

N;Alternate names: 2-oxoglutarate dehydrogenase complex chain E2;

transsuccinylase

C;Species: *Bos primigenius taurus* (cattle)

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 05-May-2000

C;Accession: S00123  
 R;Bradford, A.P.; Aitken, A.; Beg, F.; Cook, K.G.; Yeaman, S.J.  
 FEBS Lett. 222, 211-214, 1987  
 A;Title: Amino acid sequence surrounding the lipoic acid cofactor of bovine kidney 2-oxoglutarate dehydrogenase complex.  
 A;Reference number: S00123; MUID:88005143; PMID:3115829  
 A;Accession: S00123  
 A;Molecule type: protein  
 A;Residues: 1-16 <BRA>  
 C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology  
 C;Keywords: acyltransferase; coenzyme A; lipoamide; mitochondrion; oxidoreductase; tricarboxylic acid cycle  
 F;1-16/Domain: lipoyl/biotin-binding homology (fragment) <LPB>  
 F;5/Binding site: lipoamide (Lys) (covalent) #status experimental

Query Match 22.5%; Score 20; DB 2; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 3.9e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQP 6  
 :| | |  
 Db 8 VQVPSP 13

#### RESULT 30

D83794

hypothetical protein BH1156 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001

C;Accession: D83794

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiram, C.; Nakamura, Y.; Ogasawara, N.; Kuhara, S.; Horikoshi, K.  
 Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: D83794

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-16 <STO>

A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB04875.1; GSPDB:GN00137

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH1156

Query Match 22.5%; Score 20; DB 2; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 3.9e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MMEPQG 16  
 ||| :|  
 Db 10 MMELEG 15

#### RESULT 31

S33609

extensin - maize (fragment)

C;Species: Zea mays (maize)

C;Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999

C;Accession: S33609

R;Murphy, J.M.; Hood, E.E.

Plant Mol. Biol. 21, 885-893, 1993

A;Title: Molecular basis for extensin size heterogeneity in two maize varieties.

A;Reference number: S33609; MUID:93222485; PMID:8467081

A;Accession: S33609

A;Molecule type: protein

A;Residues: 1-17 <MUR>

C;Keywords: glycoprotein; hydroxyproline

Query Match 22.5%; Score 20; DB 2; Length 17;  
Best Local Similarity 75.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPQP 6  
||:|  
Db 13 TPKP 16

#### RESULT 32

B31769

T-cell receptor delta-2 chain J region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 05-Nov-1999

C;Accession: B31769

R;Loh, E.Y.; Cwirla, S.; Serafini, A.T.; Phillips, J.H.; Lanier, L.L.

Proc. Natl. Acad. Sci. U.S.A. 85, 9714-9718, 1988

A;Title: Human T-cell-receptor delta chain: genomic organization, diversity, and expression in populations of cells.

A;Reference number: A94221; MUID:89071766; PMID:2974163

A;Accession: B31769

A;Molecule type: DNA

A;Residues: 1-17 <LOH>

A;Cross-references: GB:L36386; NID:g540455; PIDN:AAA61108.1; PID:g540456

C;Keywords: T-cell receptor

Query Match 22.5%; Score 20; DB 2; Length 17;  
Best Local Similarity 50.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 QVMMEP 14  
|::||  
Db 12 QLIVEP 17

#### RESULT 33

S10452

hypothetical protein (bphA 5' region) - Aspergillus niger

C;Species: Aspergillus niger

C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Sep-1997

C;Accession: S10452

R;van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.;

van Balken, J.A.M.; Pouwels, P.H.; van den Hondel, C.A.M.J.J.

submitted to the EMBL Data Library, March 1990  
A;Reference number: S10452  
A;Accession: S10452  
A;Molecule type: DNA  
A;Residues: 1-18 <VAN>  
A;Cross-references: EMBL:X52521; NID:g2336; PID:g2337

Query Match 22.5%; Score 20; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 4.4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPL 7  
| |||  
Db 2 TDQPL 6

RESULT 34

I78841

thrombopoietin receptor - mouse (fragment)

C;Species: Mus sp. (mouse)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999

C;Accession: I78841

R;Alexander, W.S.; Dunn, A.R.

Oncogene 10, 795-803, 1995

A;Title: Structure and transcription of the genomic locus encoding murine c-Mpl, a receptor for thrombopoietin.

A;Reference number: I58350; MUID:95166571; PMID:7862460

A;Accession: I78841

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-18 <RES>

A;Cross-references: GB:S76842; NID:g912990; PIDN:AAB33462.1; PID:g912991

C;Genetics:

A;Gene: c-mp11

Query Match 22.5%; Score 20; DB 2; Length 18;  
Best Local Similarity 57.1%; Pred. No. 4.4e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 PQPLLQV 10  
| | | |  
Db 5 PAPFLTV 11

RESULT 35

S21288

lectin - potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 05-Dec-1998

C;Accession: S21288

R;Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.

Biochem. J. 283, 813-821, 1992

A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization, immunolocalization and effects of wounding.

A;Reference number: S21288; MUID:92272683; PMID:1590771

A;Accession: S21288

A;Molecule type: protein  
A;Residues: 1-8 <MIL>  
A;Experimental source: var. Ulster Sceptre  
C;Function:  
A;Description: may be involved in defence mechanism of the plant  
C;Keywords: hydroxyproline; lectin

Query Match 21.3%; Score 19; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQP 6  
|||  
Db 4 TPSP 7

RESULT 36

S70345

amine oxidase (copper-containing) (EC 1.4.3.6) II - *Aspergillus niger*  
(fragments)

C;Species: *Aspergillus niger*

C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998

C;Accession: S70345

R;Frebort, I.; Pec, P.; Luhova, L.; Toyama, H.; Matsushita, K.; Hirota, S.;  
Kitagawa, T.; Ueno, T.; Asano, Y.; Kato, Y.; Adachi, O.

Biochim. Biophys. Acta 1295, 59-72, 1996

A;Title: Two amine oxidases from *Aspergillus niger* AKU 3302 contain topa quinone  
as the cofactor: unusual cofactor link to the glutamyl residue occurs only at  
one of the enzymes.

A;Reference number: S70344; MUID:96283794; PMID:8679675

A;Accession: S70345

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5;6-9 <FRE>

C;Keywords: oxidoreductase

Query Match 21.3%; Score 19; DB 2; Length 9;  
Best Local Similarity 37.5%; Pred. No. 2.8e+05;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 10 VMMEPQGD 17  
|::|| :  
Db 1 VVIEPNXE 8

RESULT 37

D33098

214K exoantigen (version 1) - malaria parasite (*Plasmodium falciparum*)  
(fragments)

C;Species: *Plasmodium falciparum*

C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C;Accession: D33098

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: D33098

A;Status: preliminary

A;Molecule type: protein  
A;Residues: 1-10 <NIC>

Query Match 21.3%; Score 19; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MMEP 14  
|:|  
Db 4 MLEP 7

RESULT 38

A61007

hementin (EC 3.4.--.) - Amazon leech (fragment)

C;Species: Haementeria ghilianii (Amazon leech)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 07-May-1999

C;Accession: A61007

R;Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.

J. Chromatogr. 502, 359-369, 1990

A;Title: Purification and characterization of hementin, a fibrinogenolytic protease from the leech Haementeria ghilianii.

A;Reference number: A61007; MUID:90256973; PMID:2187898

A;Accession: A61007

A;Molecule type: protein

A;Residues: 1-10 <SWA>

C;Keywords: anticoagulant; hydrolase; saliva

Query Match 21.3%; Score 19; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.4e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 11 MMEPQGD 17  
: ||: |  
Db 3 LTEPEPD 9

RESULT 39

S42587

celF protein - Escherichia coli (fragment)

C;Species: Escherichia coli

C;Date: 25-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995

C;Accession: S42587

R;Guzzo, A.; DuBow, M.S.

Mol. Gen. Genet. 242, 455-460, 1994

A;Title: A luxAB transcriptional fusion to the cryptic celF gene of Escherichia coli displays increased luminescence in the presence of nickel.

A;Reference number: S42587; MUID:94166755; PMID:8121401

A;Accession: S42587

A;Molecule type: DNA

A;Residues: 1-11 <GUZ>

C;Genetics:

A;Gene: celF

Query Match 21.3%; Score 19; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQP 6  
|||  
Db 6 TPHP 9

RESULT 40

S21127

precorrin methyltransferase - Salmonella typhimurium

C;Species: Salmonella typhimurium

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995

C;Accession: S21127

R;Roesser, C.A.; Warren, M.J.; Santander, P.J.; Atshaves, B.P.; Ozaki, S.;  
Stolowich, N.J.; Iida, K.; Scott, A.I.

FEBS Lett. 301, 73-78, 1992

A;Title: Expression of 9 Salmonella typhimurium enzymes for cobinamide  
synthesis. Identification of the 11-methyl and 20-methyl transferases of corrin  
biosynthesis.

A;Reference number: S21127; MUID:93083628; PMID:1451790

A;Accession: S21127

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <ROE>

Query Match 21.3%; Score 19; DB 2; Length 11;  
Best Local Similarity 42.9%; Pred. No. 3.7e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQPL 7  
:| || :  
Db 4 IQQPQTI 10

RESULT 41

PN0044

protein kinase C inhibitor I - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998

C;Accession: PN0044

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of  
mouse neuroblastoma cells.

A;Reference number: PN0041

A;Accession: PN0044

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Experimental source: neuroblastoma cell

C;Comment: The molecular mass is 13,900 and the pI is 6.36. The amino-terminus  
is blocked.

C;Keywords: brain

Query Match 21.3%; Score 19; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 13 EPQGD 17

Db                   :| ||  
                    6 QPGGD 10

RESULT 42

A61309

glycoprotein hormones alpha chain - hamster (fragment)  
N;Alternate names: choriogonadotropin alpha chain; luteinizing hormone alpha chain; lutropin alpha chain; thyrotropin alpha chain  
C;Species: Cricetinae gen. sp. (hamster)  
C;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
C;Accession: A61309  
R;Glenn, S.D.; Nahm, H.S.; Greenwald, G.S.; Ward, D.N.  
Endocrinology 111, 1263-1269, 1982  
A;Title: Isolation and characterization of hamster luteinizing hormone.  
A;Reference number: A61309; MUID:83003498; PMID:6889489  
A;Accession: A61309  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-12 <GLE>  
C;Superfamily: glycoprotein hormones alpha chain  
C;Keywords: glycoprotein

Query Match                   21.3%;   Score 19;   DB 2;   Length 12;  
Best Local Similarity       75.0%;   Pred. No. 4.1e+03;  
Matches       3;   Conservative       0;   Mismatches       1;   Indels       0;   Gaps       0;

Qy               14 PQGD 17  
                  | ||  
Db               2 PBGD 5

RESULT 43

S36668

hypothetical protein 133 - Plectonema boryanum (fragment)  
C;Species: Plectonema boryanum  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 15-Oct-1999  
C;Accession: S36668  
R;Fujita, Y.; Matsumoto, H.; Takahashi, Y.; Matsubara, H.  
submitted to the EMBL Data Library, August 1992  
A;Description: Identification of the nifDK-like gene (ORF467) involved in the biosynthesis of chlorophyll in the cyanobacterium Plectonema boryanum.  
A;Reference number: S36668  
A;Accession: S36668  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-13 <FUJ>  
A;Cross-references: EMBL:D12973; NID:g216810; PIDN:BAA02348.1; PID:d1002847; PID:g216811

Query Match                   21.3%;   Score 19;   DB 2;   Length 13;  
Best Local Similarity       75.0%;   Pred. No. 4.5e+03;  
Matches       3;   Conservative       0;   Mismatches       1;   Indels       0;   Gaps       0;

Qy               3 TPQP 6  
                  || |  
Db               9 TPSP 12

RESULT 44

I54945

gene C protein - Escherichia coli (fragment)

C;Species: Escherichia coli

C;Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 08-Oct-1999

C;Accession: I54945

R;Tao, T.; Bourne, J.C.; Blumenthal, R.M.

J. Bacteriol. 173, 1367-1375, 1991

A;Title: A family of regulatory genes associated with type II restriction-modification systems.

A;Reference number: I54945; MUID:91139577; PMID:1995588

A;Accession: I54945

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-14 <RES>

A;Cross-references: GB:M63619; NID:g147664; PIDN:AAA24555.1; PID:g147665

Query Match 21.3%; Score 19; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 4.9e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LLQVMME 13  
| :|:|  
Db 1 LKEVIME 7

RESULT 45

A39239

actin 8 - slime mold (Dictyostelium discoideum) (fragment)

C;Species: Dictyostelium discoideum

C;Date: 20-Sep-1991 #sequence\_revision 20-Sep-1991 #text\_change 18-Jun-1993

C;Accession: A39239

R;Frankel, S.; Condeelis, J.; Leinwand, L.

J. Biol. Chem. 265, 17980-17987, 1990

A;Title: Expression of actin in Escherichia coli. Aggregation, solubilization, and functional analysis.

A;Reference number: A39239; MUID:91009269; PMID:2211676

A;Accession: A39239

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <FRA>

Query Match 21.3%; Score 19; DB 2; Length 14;  
Best Local Similarity 42.9%; Pred. No. 4.9e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 LLQVMME 13  
: |:| |  
Db 1 MTQIMFE 7

RESULT 46

S12904

protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)

C;Species: Pisaster ochraceus

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Aug-1997  
C;Accession: S12904  
R;Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.  
FEBS Lett. 273, 223-226, 1990  
A;Title: Identification of the sites in myelin basic protein that are  
phosphorylated by meiosis-activated protein kinase p44(mpk).  
A;Reference number: S12904; MUID:91032186; PMID:1699809  
A;Accession: S12904  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-14 <SAN>  
C;Keywords: phosphotransferase

Query Match 21.3%; Score 19; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 4.9e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QTPQP 6  
: || |  
Db 6 RTPPP 10

RESULT 47

A56891  
gamma 1 gliadin - wheat (fragment)  
C;Species: Triticum sp. (wheat)  
C;Date: 08-Dec-1995 #sequence\_revision 08-Dec-1995 #text\_change 08-Dec-1995  
C;Accession: A56891  
R;Sjostrom, H.; Friis, S.U.; Noren, O.; Anthonsen, D.  
Clin. Chim. Acta 207, 227-237, 1992  
A;Title: Purification and characterisation of antigenic gliadins in coeliac  
disease.  
A;Reference number: A56891; MUID:93009000; PMID:1395028  
A;Contents: Kadett  
A;Accession: A56891  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <SJO>  
A;Note: sequence extracted from NCBI backbone (NCBIP:119387)

Query Match 21.3%; Score 19; DB 2; Length 15;  
Best Local Similarity 28.6%; Pred. No. 5.3e+03;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 10 VMMEPQG 16  
: :: | |  
Db 2 IQVDPSG 8

RESULT 48

F44823  
synaptosomal-associated protein SNAP-25 peptide 9 - rabbit (fragment)  
N;Alternate names: superprotein peptide 9  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Jun-1996  
C;Accession: F44823  
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.

J. Neurosci. 11, 3412-3421, 1991

A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is identical to SNAP-25, a protein of synaptic terminals.

A;Reference number: A44823; MUID:92044785; PMID:1941090

A;Accession: F44823

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <LOE>

A;Experimental source: visual tissue

A;Note: sequence extracted from NCBI backbone (NCBIP:64316)

C;Keywords: membrane trafficking

Query Match 21.3%; Score 19; DB 2; Length 15;  
Best Local Similarity 36.4%; Pred. No. 5.3e+03;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 7 LLQVMMEPQGD 17  
:|:|:| | |  
Db 1 MLQLVEESSKD 11

#### RESULT 49

A24099

crystal protein, 28K - *Bacillus thuringiensis* (fragment)

C;Species: *Bacillus thuringiensis*

C;Date: 22-Jul-1987 #sequence\_revision 22-Jul-1987 #text\_change 20-Jun-2000

C;Accession: A24099

R;Chestukhina, G.G.; Zalunin, I.A.; Kostina, L.I.; Bormatova, M.E.; Klepikova, F.S.; Khodova, O.M.; Stepanov, V.M.

FEBS Lett. 190, 345-348, 1985

A;Title: Structural features of crystal-forming proteins produced by *Bacillus thuringiensis* subspecies *israelensis*.

A;Reference number: A91347

A;Accession: A24099

A;Molecule type: protein

A;Residues: 1-16 <CHE>

Query Match 21.3%; Score 19; DB 2; Length 16;  
Best Local Similarity 33.3%; Pred. No. 5.7e+03;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 PLLQVMMEP 14  
|| : : |  
Db 8 PLQDIKVNVP 16

#### RESULT 50

PH0763

T-cell receptor beta chain (F15) - mouse (fragment)

C;Species: *Mus musculus* (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999

C;Accession: PH0763

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-restricted cytotoxic T lymphocyte clones specific for a *Plasmodium*

berghei nonapeptide: implications for T cell allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0763

A;Molecule type: mRNA

A;Residues: 1-16 <CAS>

A;Cross-references: EMBL:X60857; NID:g50933; PIDN:CAA43247.1; PID:g50934

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 21.3%; Score 19; DB 2; Length 16;

Best Local Similarity 75.0%; Pred. No. 5.7e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 14 PQGD 17

|||:

Db 6 PQGN 9

Search completed: July 4, 2004, 04:47:14

Job time : 15.0672 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:45:52 ; Search time 33.3657 Seconds  
(without alignments)  
158.601 Million cell updates/sec

Title: US-09-641-802-2  
Perfect score: 89  
Sequence: 1 LQTPQPLLQVMMEPQGD 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 203405

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.						

1	89	100.0	17	14	US-10-281-652-2	Sequence 2, Appli
2	33	37.1	12	14	US-10-286-457-195	Sequence 195, App
3	33	37.1	15	14	US-10-281-652-34	Sequence 34, Appl
4	30	33.7	16	12	US-10-346-162-130	Sequence 130, App
5	29	32.6	9	13	US-10-017-327-3	Sequence 3, Appli
6	29	32.6	10	14	US-10-073-054-20	Sequence 20, Appl
7	29	32.6	13	12	US-10-469-101-53	Sequence 53, Appl
8	29	32.6	18	9	US-09-864-761-40147	Sequence 40147, A
9	28	31.5	9	12	US-10-013-312-33	Sequence 33, Appl
10	28	31.5	9	12	US-10-013-312-412	Sequence 412, App
11	28	31.5	9	12	US-10-013-312-502	Sequence 502, App
12	28	31.5	9	12	US-10-013-312-605	Sequence 605, App
13	28	31.5	9	12	US-10-013-312-1358	Sequence 1358, Ap
14	28	31.5	9	12	US-10-013-312-1522	Sequence 1522, Ap
15	28	31.5	9	12	US-10-013-312-1598	Sequence 1598, Ap
16	28	31.5	9	12	US-10-013-312-1693	Sequence 1693, Ap
17	28	31.5	9	12	US-10-013-312-1721	Sequence 1721, Ap
18	28	31.5	9	12	US-10-013-312-1810	Sequence 1810, Ap
19	28	31.5	9	12	US-10-013-312-1928	Sequence 1928, Ap
20	28	31.5	9	12	US-10-013-312-1983	Sequence 1983, Ap
21	28	31.5	9	12	US-10-013-312-2020	Sequence 2020, Ap
22	28	31.5	10	9	US-09-908-322-53	Sequence 53, Appl
23	28	31.5	10	10	US-09-783-931-53	Sequence 53, Appl
24	28	31.5	10	12	US-10-013-312-82	Sequence 82, Appl
25	28	31.5	10	12	US-10-013-312-196	Sequence 196, App
26	28	31.5	10	12	US-10-013-312-459	Sequence 459, App
27	28	31.5	10	12	US-10-013-312-560	Sequence 560, App
28	28	31.5	10	12	US-10-013-312-690	Sequence 690, App
29	28	31.5	10	12	US-10-013-312-2072	Sequence 2072, Ap
30	28	31.5	10	12	US-10-013-312-2241	Sequence 2241, Ap
31	28	31.5	10	12	US-10-013-312-2432	Sequence 2432, Ap
32	28	31.5	10	12	US-10-013-312-2450	Sequence 2450, Ap
33	28	31.5	13	14	US-10-234-816-33	Sequence 33, Appl
34	28	31.5	14	14	US-10-185-425-24	Sequence 24, Appl
35	28	31.5	15	12	US-10-013-312-2620	Sequence 2620, Ap
36	28	31.5	15	12	US-10-013-312-2653	Sequence 2653, Ap
37	28	31.5	15	12	US-10-013-312-2691	Sequence 2691, Ap
38	28	31.5	15	12	US-10-013-312-2692	Sequence 2692, Ap
39	28	31.5	15	12	US-10-013-312-2781	Sequence 2781, Ap
40	28	31.5	15	12	US-10-013-312-2808	Sequence 2808, Ap
41	28	31.5	15	12	US-10-013-312-2824	Sequence 2824, Ap
42	28	31.5	16	14	US-10-161-791-195	Sequence 195, App
43	28	31.5	16	15	US-10-319-315-49	Sequence 49, Appl
44	27.5	30.9	14	10	US-09-991-225-68	Sequence 68, Appl
45	27.5	30.9	14	12	US-10-369-405-68	Sequence 68, Appl
46	27.5	30.9	18	9	US-09-984-056-95	Sequence 95, Appl
47	27.5	30.9	18	14	US-10-105-232-95	Sequence 95, Appl
48	27	30.3	10	14	US-10-185-815-89	Sequence 89, Appl
49	27	30.3	12	10	US-09-954-385-136	Sequence 136, App
50	27	30.3	15	10	US-09-749-873-125	Sequence 125, App
51	27	30.3	16	14	US-10-267-251-7	Sequence 7, Appli
52	27	30.3	16	14	US-10-299-043-2	Sequence 2, Appli
53	26.5	29.8	18	9	US-09-829-855-240	Sequence 240, App
54	26.5	29.8	18	16	US-10-607-077A-240	Sequence 240, App
55	26	29.2	8	15	US-10-376-121A-182	Sequence 182, App
56	26	29.2	8	15	US-10-376-121A-185	Sequence 185, App

57	26	29.2	9	8	US-08-344-824-282	Sequence 282, App
58	26	29.2	10	8	US-08-344-824-393	Sequence 393, App
59	26	29.2	10	10	US-09-572-404B-1161	Sequence 1161, Ap
60	26	29.2	14	10	US-09-992-665-52	Sequence 52, Appl
61	26	29.2	15	12	US-10-682-420-121	Sequence 121, App
62	26	29.2	15	12	US-10-013-312-2882	Sequence 2882, Ap
63	26	29.2	15	16	US-10-409-613-121	Sequence 121, App
64	26	29.2	15	16	US-10-442-180-121	Sequence 121, App
65	26	29.2	17	9	US-09-864-761-46994	Sequence 46994, A
66	26	29.2	17	14	US-10-138-089-18	Sequence 18, Appl
67	26	29.2	17	16	US-10-422-571-99	Sequence 99, Appl
68	26	29.2	18	8	US-08-945-038-12	Sequence 12, Appl
69	26	29.2	18	14	US-10-225-567A-1708	Sequence 1708, Ap
70	25	28.1	9	12	US-10-334-726-124	Sequence 124, App
71	25	28.1	10	12	US-10-363-791-128	Sequence 128, App
72	25	28.1	10	12	US-10-325-810-116	Sequence 116, App
73	25	28.1	12	14	US-10-193-477-146	Sequence 146, App
74	25	28.1	12	14	US-10-193-477-168	Sequence 168, App
75	25	28.1	12	15	US-10-137-867-452	Sequence 452, App
76	25	28.1	13	9	US-09-938-315-92	Sequence 92, Appl
77	25	28.1	13	9	US-09-791-378-456	Sequence 456, App
78	25	28.1	13	12	US-10-403-847-54	Sequence 54, Appl
79	25	28.1	13	12	US-10-403-847-74	Sequence 74, Appl
80	25	28.1	13	12	US-10-469-101-54	Sequence 54, Appl
81	25	28.1	13	12	US-09-791-377-456	Sequence 456, App
82	25	28.1	13	14	US-10-161-791-92	Sequence 92, Appl
83	25	28.1	13	16	US-10-412-964-35	Sequence 35, Appl
84	25	28.1	14	10	US-09-845-612B-15	Sequence 15, Appl
85	25	28.1	14	12	US-10-014-340-705	Sequence 705, App
86	25	28.1	14	16	US-10-346-058-58	Sequence 58, Appl
87	25	28.1	15	8	US-08-927-939-4	Sequence 4, Appli
88	25	28.1	15	12	US-10-682-420-119	Sequence 119, App
89	25	28.1	15	12	US-10-682-420-120	Sequence 120, App
90	25	28.1	15	16	US-10-409-613-119	Sequence 119, App
91	25	28.1	15	16	US-10-409-613-120	Sequence 120, App
92	25	28.1	15	16	US-10-442-180-119	Sequence 119, App
93	25	28.1	15	16	US-10-442-180-120	Sequence 120, App
94	25	28.1	16	12	US-10-346-162-30	Sequence 30, Appl
95	25	28.1	16	14	US-10-225-567A-898	Sequence 898, App
96	25	28.1	17	12	US-10-609-217-272	Sequence 272, App
97	25	28.1	17	12	US-10-632-388-272	Sequence 272, App
98	25	28.1	17	12	US-10-651-723-272	Sequence 272, App
99	25	28.1	17	12	US-10-645-761-272	Sequence 272, App
100	25	28.1	17	16	US-10-666-696-272	Sequence 272, App

#### ALIGNMENTS

#### RESULT 1

US-10-281-652-2

; Sequence 2, Application US/10281652

; Publication No. US20030091606A1

; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

```
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-2
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Query Match          100.0%; Score 89; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 LQTPQPLLQVMMEPQGD 17
          |||||
Db      1 LQTPQPLLQVMMEPQGD 17
```

## RESULT 2

US-10-286-457-195

```
; Sequence 195, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND
THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 195
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide
libraries, based on
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-195
```

```
Query Match          37.1%; Score 33; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LQTPQP 6  
| | | | |  
Db 2 LQTPQP 7

RESULT 3

US-10-281-652-34  
; Sequence 34, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-34

Query Match 37.1%; Score 33; DB 14; Length 15;  
Best Local Similarity 53.8%; Pred. No. 2.3e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14  
| | | | : | |  
Db 3 QPPQPLPPTVMFP 15

RESULT 4

US-10-346-162-130  
; Sequence 130, Application US/10346162  
; Publication No. US20030224390A1  
; GENERAL INFORMATION:  
; APPLICANT: KARO BIO USA, INC.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: BARNETT, Thomas R.  
; APPLICANT: BUEHRER, Benjamin  
; TITLE OF INVENTION: METHOD OF IDENTIFYING CONFORMATION-SENSITIVE BINDING  
PEPTIDES AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: PAIGE=1H  
; CURRENT APPLICATION NUMBER: US/10/346,162

; CURRENT FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: US 09/614,865  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 09/860,688  
; PRIOR FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 268  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 130  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-346-162-130

Query Match 33.7%; Score 30; DB 12; Length 16;  
Best Local Similarity 45.5%; Pred. No. 7e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 PLLQVMMEPQG 16  
||| :: ||  
Db 5 PLLMALLAPPG 15

#### RESULT 5

US-10-017-327-3

; Sequence 3, Application US/10017327  
; Publication No. US20020155471A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles A. Nicolette  
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS AND  
; TITLE OF INVENTION: METHODS FOR USING SAME  
; FILE REFERENCE: GZ 2101.20  
; CURRENT APPLICATION NUMBER: US/10/017,327  
; CURRENT FILING DATE: 2001-12-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-327-3

Query Match 32.6%; Score 29; DB 13; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.2e+06;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LQVMMEP 14  
||::|||  
Db 2 LQLLMEP 8

#### RESULT 6

US-10-073-054-20

; Sequence 20, Application US/10073054  
; Publication No. US20030167485A1  
; GENERAL INFORMATION:

```
; APPLICANT: Garvan Institute of Medical Research
; APPLICANT: HERZOG, Herbert
; TITLE OF INVENTION: No. US20030167485A1 G-protein coupled receptor-encoding
gene and diagnostic uses
; TITLE OF INVENTION: therefor
; FILE REFERENCE: 1871-132 (93702-CIP/MRO)
; CURRENT APPLICATION NUMBER: US/10/073,054
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/308,696
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00805
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: AU P09386
; PRIOR FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: N-terminal peptide
US-10-073-054-20
```

```
Query Match          32.6%; Score 29; DB 14; Length 10;
Best Local Similarity 85.7%; Pred. No. 6.1e+02;
Matches      6; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy      . 3 TPQPLLQ 9
          ||| |||
Db      2 TPQSLQ 8
```

```
RESULT 7
US-10-469-101-53
; Sequence 53, Application US/10469101
; Publication No. US20040071688A1
; GENERAL INFORMATION:
; APPLICANT: CARR, Francis J.
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: MODIFIED THROMBOPOIETIN WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-109
; CURRENT APPLICATION NUMBER: US/10/469,101
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: EP 01104702.4
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: PCT/EP02/01931
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-469-101-53
```

Query Match 32.6%; Score 29; DB 12; Length 13;  
Best Local Similarity 50.0%; Pred. No. 8.1e+02;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQG 16  
| | | : | | |  
Db 1 QSLLGTLPPQG 12

RESULT 8

US-09-864-761-40147

; Sequence 40147, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES  
USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40147
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005343.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
US-09-864-761-40147
```

```
Query Match          32.6%; Score 29; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      5 QPLLQV 10
        |||||
Db      3 QPLLQV 8
```

#### RESULT 9

```
US-10-013-312-33
; Sequence 33, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-33
```

```
Query Match          31.5%; Score 28; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches      4; Conservative      2; Mismatches      1; Indels      0; Gaps      0;
```

Qy 3 TPQPLLQ 9  
|||::|  
Db 3 TPSPIIQ 9

RESULT 10

US-10-013-312-412

; Sequence 412, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 412  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-412

Query Match 31.5%; Score 28; DB 12; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 1 TPSPIIQ 7

RESULT 11

US-10-013-312-502

; Sequence 502, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 502  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-502

Query Match 31.5%; Score 28; DB 12; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 1 TPSPIIQ 7

RESULT 12

US-10-013-312-605

; Sequence 605, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 605  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-605

Query Match 31.5%; Score 28; DB 12; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 1 TPSPIIQ 7

RESULT 13

US-10-013-312-1358

; Sequence 1358, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE

```
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1358
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1358
```

```
Query Match          31.5%; Score 28; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches      4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      3 TPQPLLQ 9
        |||::|
Db      1 TPSPIIQ 7
```

#### RESULT 14

```
US-10-013-312-1522
; Sequence 1522, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1522
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1522
```

```
Query Match          31.5%; Score 28; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches      4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      3 TPQPLLQ 9
        |||::|
Db      2 TPSPIIQ 8
```

RESULT 15

US-10-013-312-1598

; Sequence 1598, Application US/10013312

; Publication No. US20030223990A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA

; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITZ, AYA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED

; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER

; FILE REFERENCE: 51158-20063.00

; CURRENT APPLICATION NUMBER: US/10/013,312

; CURRENT FILING DATE: 2002-05-30

; NUMBER OF SEQ ID NOS: 3005

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1598

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-013-312-1598

Query Match 31.5%; Score 28; DB 12; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.2e+06;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9

|||::|

Db 1 TPSPIIQ 7

RESULT 16

US-10-013-312-1693

; Sequence 1693, Application US/10013312

; Publication No. US20030223990A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA

; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITZ, AYA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED

; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER

; FILE REFERENCE: 51158-20063.00

; CURRENT APPLICATION NUMBER: US/10/013,312

; CURRENT FILING DATE: 2002-05-30

; NUMBER OF SEQ ID NOS: 3005

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1693

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-013-312-1693

Query Match 31.5%; Score 28; DB 12; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 1 TPSPIIQ 7

RESULT 17

US-10-013-312-1721  
; Sequence 1721, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1721  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-1721

Query Match 31.5%; Score 28; DB 12; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 1 TPSPIIQ 7

RESULT 18

US-10-013-312-1810  
; Sequence 1810, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312

; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1810  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-1810

Query Match 31.5%; Score 28; DB 12; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 1 TPSPIIQ 7

RESULT 19

US-10-013-312-1928  
; Sequence 1928, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1928  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-1928

Query Match 31.5%; Score 28; DB 12; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 1 TPSPIIQ 7

RESULT 20

US-10-013-312-1983  
; Sequence 1983, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR

```
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1983
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1983
```

```
Query Match          31.5%; Score 28; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches      4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      3 TPQPLLQ 9
        |||::|
Db      1 TPSPIIQ 7
```

#### RESULT 21

```
US-10-013-312-2020
; Sequence 2020, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2020
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2020
```

```
Query Match          31.5%; Score 28; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches      4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      3 TPQPLLQ 9
        |||::|
```

## RESULT 22

US-09-908-322-53

; Sequence 53, Application US/09908322

; Patent No. US20020107194A1

; GENERAL INFORMATION:

; APPLICANT: Ish-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace

; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF  
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/908,322  
; FILING DATE: 17-Jul-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-123

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 53:

US-09-908-322-53

Query Match 31.5%; Score 28; DB 9; Length 10;

Best Local Similarity 50.0%; Pred. No. 8.7e+02;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 PQPLLQVMME 13  
| | | | : : |  
Db 1 PQPLVRTEQE 10

RESULT 23

US-09-783-931-53

; Sequence 53, Application US/09783931

; Publication No. US20030073620A1

; GENERAL INFORMATION:

; APPLICANT: Ish-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace

; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS  
; AND FRAGMENTS

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/783,931  
; FILING DATE: 15-Feb-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Antler, Adriane M.  
; REGISTRATION NUMBER: 32,605  
; REFERENCE/DOCKET NUMBER: 7326-122

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 53:

US-09-783-931-53

Query Match 31.5%; Score 28; DB 10; Length 10;  
Best Local Similarity 50.0%; Pred. No. 8.7e+02;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 PQPLLQVMME 13  
|||::|  
Db 1 PQPLVRTEQE 10

RESULT 24

US-10-013-312-82  
; Sequence 82, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 82  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-82

Query Match 31.5%; Score 28; DB 12; Length 10;  
Best Local Similarity 57.1%; Pred. No. 8.7e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 3 TPSPIIQ 9

RESULT 25

US-10-013-312-196  
; Sequence 196, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 196  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-196

Query Match 31.5%; Score 28; DB 12; Length 10;  
Best Local Similarity 57.1%; Pred. No. 8.7e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 2 TPSPIIQ 8

RESULT 26

US-10-013-312-459  
; Sequence 459, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 459  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-459

Query Match 31.5%; Score 28; DB 12; Length 10;  
Best Local Similarity 57.1%; Pred. No. 8.7e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 2 TPSPIIQ 8

RESULT 27

US-10-013-312-560  
; Sequence 560, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 560  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-560

Query Match 31.5%; Score 28; DB 12; Length 10;  
Best Local Similarity 57.1%; Pred. No. 8.7e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 2 TPSPIIQ 8

RESULT 28

US-10-013-312-690

; Sequence 690, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 690  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-690

Query Match 31.5%; Score 28; DB 12; Length 10;  
Best Local Similarity 57.1%; Pred. No. 8.7e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 2 TPSPIIQ 8

RESULT 29

US-10-013-312-2072

; Sequence 2072, Application US/10013312

; Publication No. US20030223990A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA

; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITZ, AYA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED

; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER

; FILE REFERENCE: 51158-20063.00

; CURRENT APPLICATION NUMBER: US/10/013,312

; CURRENT FILING DATE: 2002-05-30

; NUMBER OF SEQ ID NOS: 3005

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2072

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-013-312-2072

Query Match 31.5%; Score 28; DB 12; Length 10;

Best Local Similarity 57.1%; Pred. No. 8.7e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9

|||::|

Db 2 TPSPIIQ 8

RESULT 30

US-10-013-312-2241

; Sequence 2241, Application US/10013312

; Publication No. US20030223990A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA

; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITZ, AYA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED

; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER

; FILE REFERENCE: 51158-20063.00

; CURRENT APPLICATION NUMBER: US/10/013,312

; CURRENT FILING DATE: 2002-05-30

; NUMBER OF SEQ ID NOS: 3005

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2241

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-013-312-2241

Query Match 31.5%; Score 28; DB 12; Length 10;  
Best Local Similarity 57.1%; Pred. No. 8.7e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 2 TPSPIIQ 8

RESULT 31

US-10-013-312-2432

; Sequence 2432, Application US/10013312

; Publication No. US20030223990A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA

; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITZ, AYA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED

; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER

; FILE REFERENCE: 51158-20063.00

; CURRENT APPLICATION NUMBER: US/10/013,312

; CURRENT FILING DATE: 2002-05-30

; NUMBER OF SEQ ID NOS: 3005

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2432

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-013-312-2432

Query Match 31.5%; Score 28; DB 12; Length 10;  
Best Local Similarity 57.1%; Pred. No. 8.7e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 1 TPSPIIQ 7

RESULT 32

US-10-013-312-2450

; Sequence 2450, Application US/10013312

; Publication No. US20030223990A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA

; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITZ, AYA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED

; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER

; FILE REFERENCE: 51158-20063.00

; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2450  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-2450

Query Match 31.5%; Score 28; DB 12; Length 10;  
Best Local Similarity 57.1%; Pred. No. 8.7e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 2 TPSPIIQ 8

RESULT 33

US-10-234-816-33  
; Sequence 33, Application US/10234816  
; Publication No. US20030157514A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL PLECKSTRIN HOMOLOGY  
DOMAIN AND PROLINE  
; TITLE OF INVENTION: RICH DOMAIN CONTAINING ADAPTER PROTEIN, PMN29  
; FILE REFERENCE: D0117 NP  
; CURRENT APPLICATION NUMBER: US/10/234,816  
; CURRENT FILING DATE: 2002-09-04  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-234-816-33

Query Match 31.5%; Score 28; DB 14; Length 13;  
Best Local Similarity 57.1%; Pred. No. 1.2e+03;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQPLL 8  
:|::|:  
Db 5 ETPRPLM 11

RESULT 34

US-10-185-425-24  
; Sequence 24, Application US/10185425  
; Publication No. US20030053984A1  
; GENERAL INFORMATION:  
; APPLICANT: Apotech Research and Development Ltd.  
; APPLICANT: Tschopp, Jurg  
; APPLICANT: Schneider, Pascal  
; APPLICANT: Holler, Nils

```
; TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or
Pentamer of
; TITLE OF INVENTION: Recombinant Fusion Proteins
; FILE REFERENCE: 1708.001US1
; CURRENT APPLICATION NUMBER: US/10/185,425
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: PCT/EP00/13032
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: DE 199 63 859.4
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Linker
US-10-185-425-24
```

```
Query Match          31.5%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches      6; Conservative 1; Mismatches      5; Indels      0; Gaps      0;
```

```
Qy      4 PQPLLQVMMEPQ 15
        ||| |  ||:
Db      3 PQPKPQPKPEPE 14
```

#### RESULT 35

US-10-013-312-2620

```
; Sequence 2620, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2620
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2620
```

```
Query Match          31.5%; Score 28; DB 12; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches      4; Conservative 2; Mismatches      1; Indels      0; Gaps      0;
```

Qy 3 TPQPLLQ 9  
|| |::|  
Db 7 TPSPIIQ 13

RESULT 36

US-10-013-312-2653

; Sequence 2653, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2653  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-2653

Query Match 31.5%; Score 28; DB 12; Length 15;  
Best Local Similarity 57.1%; Pred. No. 1.3e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|| |::|  
Db 1 TPSPIIQ 7

RESULT 37

US-10-013-312-2691

; Sequence 2691, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2691

; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-2691

Query Match 31.5%; Score 28; DB 12; Length 15;  
Best Local Similarity 57.1%; Pred. No. 1.3e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 8 TPSPIIQ 14

RESULT 38

US-10-013-312-2692  
; Sequence 2692, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2692  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-2692

Query Match 31.5%; Score 28; DB 12; Length 15;  
Best Local Similarity 57.1%; Pred. No. 1.3e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 6 TPSPIIQ 12

RESULT 39

US-10-013-312-2781  
; Sequence 2781, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO

```
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED .
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2781
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2781
```

```
Query Match          31.5%; Score 28; DB 12; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches      4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      3 TPQPLLQ 9
        |||::|
Db      7 TPSPIIQ 13
```

RESULT 40

```
US-10-013-312-2808
; Sequence 2808, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2808
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2808
```

```
Query Match          31.5%; Score 28; DB 12; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches      4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      3 TPQPLLQ 9
        |||::|
Db      2 TPSPIIQ 8
```

RESULT 41

US-10-013-312-2824

; Sequence 2824, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2824  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-2824

Query Match 31.5%; Score 28; DB 12; Length 15;  
Best Local Similarity 57.1%; Pred. No. 1.3e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|||::|  
Db 6 TPSPIIQ 12

RESULT 42

US-10-161-791-195

; Sequence 195, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/10/161,791
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/602,999
;   FILING DATE:  16-FEB-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Misrock, S. Leslie
;   REGISTRATION NUMBER:  18,872
;   REFERENCE/DOCKET NUMBER:  1101-202
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 790-9090
;   TELEFAX:  (212) 869-9741/8864
;   TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  195:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  16 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-10-161-791-195

```

```

Query Match          31.5%;  Score 28;  DB 14;  Length 16;
Best Local Similarity 41.7%;  Pred. No. 1.4e+03;
Matches      5;  Conservative  2;  Mismatches  5;  Indels    0;  Gaps    0;

```

```

Qy      3 TPQPLLQVMMEP 14
        ||:| :  | |
Db      4 TPRPAVPQRMNP 15

```

#### RESULT 43

```

US-10-319-315-49
; Sequence 49, Application US/10319315
; Publication No. US20030219774A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN NEUROTRANSMITTER TRANSPORTER
; FILE REFERENCE: D0205 NP
; CURRENT APPLICATION NUMBER: US/10/319,315
; CURRENT FILING DATE:  2002-12-13
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-319-315-49

```

```

Query Match          31.5%;  Score 28;  DB 15;  Length 16;
Best Local Similarity 50.0%;  Pred. No. 1.4e+03;
Matches      5;  Conservative  2;  Mismatches  3;  Indels    0;  Gaps    0;

```

```

Qy      6 PLLQVMMEPQ 15

```

Db                    | | |::||  
                      3 PKLDKMLDPQ 12

RESULT 44

US-09-991-225-68

; Sequence 68, Application US/09991225  
; Publication No. US20030153063A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11,  
EXPRESSED HIGHLY IN  
; TITLE OF INVENTION: HEART AND VARIANTS THEREOF  
; FILE REFERENCE: D0075.NP  
; CURRENT APPLICATION NUMBER: US/09/991,225  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/249,613  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/257,611  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/305,818  
; PRIOR FILING DATE: 2001-07-16  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 68  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-991-225-68

Query Match                    30.9%; Score 27.5; DB 10; Length 14;  
Best Local Similarity       53.8%; Pred. No. 1.5e+03;  
Matches       7; Conservative       1; Mismatches       4; Indels       1; Gaps       1;

Qy                    5 QPLLQVM-MEPQG 16  
                      || : | ||| |  
Db                    2 QPSISVSEMEPNG 14

RESULT 45

US-10-369-405-68

; Sequence 68, Application US/10369405  
; Publication No. US20030224400A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, AND  
VARIANTS  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: D0075A CIP  
; CURRENT APPLICATION NUMBER: US/10/369,405  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: U.S. 60/249,613  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: U.S. 09/991,225  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: U.S. 60/257,611  
; PRIOR FILING DATE: 2000-12-21

; PRIOR APPLICATION NUMBER: U.S. 60/305,818  
; PRIOR FILING DATE: 2001-07-16  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 68  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-369-405-68

Query Match 30.9%; Score 27.5; DB 12; Length 14;  
Best Local Similarity 53.8%; Pred. No. 1.5e+03;  
Matches 7; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 5 QPLLQVM-MEPQG 16  
|| : | ||| |  
Db 2 QPSISVSEMEPNG 14

RESULT 46

US-09-984-056-95

; Sequence 95, Application US/09984056  
; Patent No. US20020120106A1  
; GENERAL INFORMATION:  
; APPLICANT: BOGOCH, SAMUEL  
; APPLICANT: BOGOCH, ELENORE S.  
; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLIKINS AND METHODS OF USE  
; FILE REFERENCE: 09425-46903  
; CURRENT APPLICATION NUMBER: US/09/984,056  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: 60/303,396  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/278,761  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 09/146,755  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: 09/817,144  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 08/198,139  
; PRIOR FILING DATE: 1994-02-17  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn 2.1  
; SEQ ID NO 95  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Bacillus anthracis  
US-09-984-056-95

Query Match 30.9%; Score 27.5; DB 9; Length 18;  
Best Local Similarity 41.2%; Pred. No. 1.9e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

Qy 1 LQTPQPLLQVMMEPQGD 17  
|| | |: ||: |  
Db 3 LQIPPPPI-----EPKKD 14

RESULT 47

US-10-105-232-95

; Sequence 95, Application US/10105232  
 ; Publication No. US20030180328A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOGOCH, SAMUEL  
 ; APPLICANT: BOGOCH, ELENORE S.  
 ; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS  
 ; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS  
 ; FILE REFERENCE: 09425-46904  
 ; CURRENT APPLICATION NUMBER: US/10/105,232  
 ; CURRENT FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: 60/303,396  
 ; PRIOR FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: 60/278,761  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: 09/146,755  
 ; PRIOR FILING DATE: 1998-09-04  
 ; PRIOR APPLICATION NUMBER: 09/817,144  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: 08/198,139  
 ; PRIOR FILING DATE: 1994-02-17  
 ; NUMBER OF SEQ ID NOS: 535  
 ; SOFTWARE: PatentIn 2.1  
 ; SEQ ID NO 95  
 ; LENGTH: 18  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus anthracis

US-10-105-232-95

Query Match 30.9%; Score 27.5; DB 14; Length 18;  
 Best Local Similarity 41.2%; Pred. No. 1.9e+03;  
 Matches 7; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

Qy 1 LQTPQPLLQVMMEPQGD 17  
 ||| | : ||: |  
 Db 3 LQIPPPPI-----EPKKD 14

RESULT 48

US-10-185-815-89

; Sequence 89, Application US/10185815  
 ; Publication No. US20030096354A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Elan Corporation, plc  
 ; APPLICANT: O'Mahony, Daniel  
 ; APPLICANT: Lambkin, Imelda  
 ; APPLICANT: Higgins, Lisa  
 ; TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands  
 ; FILE REFERENCE: E1067-20093  
 ; CURRENT APPLICATION NUMBER: US/10/185,815  
 ; CURRENT FILING DATE: 2002-10-09  
 ; PRIOR APPLICATION NUMBER: 60/302,591  
 ; PRIOR FILING DATE: 2001-07-02  
 ; NUMBER OF SEQ ID NOS: 99  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 89

; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Segment of CAPHI beta casein precursor  
US-10-185-815-89

Query Match 30.3%; Score 27; DB 14; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QTPQPL 7  
| ||||  
Db 5 QPPQPL 10

RESULT 49

US-09-954-385-136

; Sequence 136, Application US/09954385  
; Publication No. US20030100467A1  
; GENERAL INFORMATION:  
; APPLICANT: Aehle, Wolfgang  
; APPLICANT: Baldwin, Toby L.  
; APPLICANT: Van Gastel, Franciscus J.C.  
; APPLICANT: Janssen, Giselle G.  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Wang, Huaming  
; APPLICANT: Winetzky, Deborah S.  
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
; TITLE OF INVENTION: Complexes  
; FILE REFERENCE: GC690  
; CURRENT APPLICATION NUMBER: US/09/954,385  
; CURRENT FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 433  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 136  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: binding peptide  
US-09-954-385-136

Query Match 30.3%; Score 27; DB 10; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.5e+03;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQPLLQ 9  
|| |||:  
Db 6 TPPPLLR 12

RESULT 50

US-09-749-873-125

; Sequence 125, Application US/09749873  
; Publication No. US20030023045A1  
; GENERAL INFORMATION:

```

;      APPLICANT: OHTOMO, Toshihiko
;              SATO, Koh
;              TSUCHIYA, Masayuki
;      TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                          MEDULLOBLASTOMA CELLS
;      NUMBER OF SEQUENCES: 132
;      CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Foley & Lardner
;              STREET: 3000 K Street, N.W., Suite 500
;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: USA
;              ZIP: 20007-5109
;      COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/749,873
;              FILING DATE: 29-Dec-2000
;              CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/646,265
;              FILING DATE: 1996-09-09
;              APPLICATION NUMBER: JP 5-291078
;              FILING DATE: 19-NOV-1993
;      ATTORNEY/AGENT INFORMATION:
;              NAME: WEGNER, Harold C.
;              REGISTRATION NUMBER: 25,258
;              REFERENCE/DOCKET NUMBER: 53466/184
;      TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;      INFORMATION FOR SEQ ID NO: 125:
;              SEQUENCE CHARACTERISTICS:
;                  LENGTH: 15 amino acids
;                  TYPE: amino acid
;                  TOPOLOGY: linear
;              MOLECULE TYPE: protein
;              SEQUENCE DESCRIPTION: SEQ ID NO: 125:
US-09-749-873-125

```

```

Query Match          30.3%;  Score 27;  DB 10;  Length 15;
Best Local Similarity 57.1%;  Pred. No. 1.9e+03;
Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy      2 QTPQPLL 8
        |:|:|:
Db      8 QSPKPLI 14

```

```

Search completed: July  4, 2004, 05:12:23
Job time : 35.3657 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:51 ; Search time 28.9254 Seconds  
(without alignments)  
185.436 Million cell updates/sec

Title: US-09-641-802-2  
Perfect score: 89  
Sequence: 1 LQTPQPLLQVMMEPQGD 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 5664

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description
-----					

1	32	36.0	18	5	Q9TWM9	Q9twm9 tetrahymena
2	28	31.5	17	10	Q7Y0I3	Q7y0i3 zea mays su
3	27	30.3	16	8	Q8MC25	Q8mc25 sonneratia
4	27	30.3	16	8	Q8MC39	Q8mc39 ammannia ba
5	27	30.3	16	8	Q8LVE1	Q8lve1 punica gran
6	27	30.3	16	8	Q8MC53	Q8mc53 woodfordia
7	27	30.3	16	8	Q8MC17	Q8mc17 ludwigia hy
8	27	30.3	16	8	Q8LVE2	Q8lve2 lythrum sal
9	27	30.3	16	8	Q8LVE0	Q8lve0 trapa maxim
10	27	30.3	16	8	Q8MET2	Q8met2 saxifraga s
11	27	30.3	16	8	Q8MC45	Q8mc45 decodon ver
12	27	30.3	16	8	Q8MC21	Q8mc21 combretum w
13	27	30.3	16	8	Q8MC51	Q8mc51 cuphea lanc
14	27	30.3	16	8	Q8MC83	Q8mc33 rotala indi
15	27	30.3	16	8	Q8MC19	Q8mc19 quisqualis
16	27	30.3	16	8	Q8MC49	Q8mc49 pemphis aci
17	27	30.3	16	8	Q8MC27	Q8mc27 lagerstroem
18	27	30.3	16	8	Q8MET0	Q8met0 cercidiphyll
19	27	30.3	16	8	Q8MC23	Q8mc23 sonneratia
20	27	30.3	16	8	Q8MC41	Q8mc41 nesaea lued
21	27	30.3	16	8	Q8MC15	Q8mc15 fuchsia hyb
22	27	30.3	16	8	Q8MC43	Q8mc43 sonneratia
23	27	30.3	16	8	Q8MC47	Q8mc47 peplis port
24	27	30.3	16	8	Q8MC37	Q8mc37 lawsonia in
25	27	30.3	16	8	Q8MC29	Q8mc29 duabanga gr
26	27	30.3	16	8	Q8MC31	Q8mc31 lagerstroem
27	27	30.3	16	8	Q8MES8	Q8mes8 daphniphyll
28	27	30.3	16	8	Q8MC35	Q8mc35 heimia myrt
29	27	30.3	17	8	Q9XQN9	Q9xqn9 sinapis alb
30	26	29.2	17	13	Q90XE2	Q90xe2 gallus gall
31	25	28.1	16	4	Q9UCH1	Q9uch1 homo sapien
32	25	28.1	16	6	Q9TRB4	Q9trb4 bos taurus
33	25	28.1	17	2	Q9APT4	Q9apt4 pseudomonas
34	25	28.1	18	2	Q9R5F6	Q9r5f6 helicobacte
35	23	25.8	11	2	Q44237	Q44237 anabaena sp
36	23	25.8	13	4	Q9UEE2	Q9uee2 homo sapien
37	23	25.8	16	4	Q96RT5	Q96rt5 homo sapien
38	23	25.8	16	10	Q84RM4	Q84rm4 boea crassi
39	23	25.8	17	2	Q7X3X0	Q7x3x0 streptomyce
40	23	25.8	18	7	Q30216	Q30216 homo sapien
41	22	24.7	12	11	Q8CG32	Q8cg32 rattus sp.
42	22	24.7	13	11	Q88176	Q88176 mus musculu
43	22	24.7	13	11	Q8CIW3	Q8ciw3 mus musculu
44	22	24.7	16	4	Q9NNZ2	Q9nnz2 homo sapien
45	22	24.7	18	16	Q81CS8	Q81cs8 bacillus ce
46	21	23.6	8	8	Q9T2Y3	Q9t2y3 begonia for
47	21	23.6	10	11	Q7TSC5	Q7tsc5 mus musculu
48	21	23.6	15	2	Q9X637	Q9x637 klebsiella
49	21	23.6	15	2	Q9X635	Q9x635 escherichia
50	21	23.6	16	4	Q9UQS4	Q9uqs4 homo sapien
51	21	23.6	16	15	Q7SM54	Q7sm54 human t-lym
52	21	23.6	17	12	Q8V9K6	Q8v9k6 human papil
53	21	23.6	17	15	Q9EL24	Q9el24 human immun
54	21	23.6	18	2	Q9R5S8	Q9r5s8 treponema d
55	20	22.5	8	2	Q8GMM5	Q8gmm5 acinetobact
56	20	22.5	10	4	Q9UNF2	Q9unf2 homo sapien
57	20	22.5	13	12	Q81769	Q81769 hepatitis c

58	20	22.5	15	7	Q9TNQ1	Q9tnq1 mus sp. bet
59	20	22.5	15	10	Q9S8N8	Q9s8n8 hordeum vul
60	20	22.5	15	11	Q9QV72	Q9qv72 mus sp. int
61	20	22.5	16	5	Q9TWK1	Q9twk1 mytilus edu
62	20	22.5	16	6	Q9TR99	Q9tr99 canis famil
63	20	22.5	16	8	Q9T2R0	Q9t2r0 solanum tub
64	20	22.5	16	16	Q9KDQ5	Q9kdq5 bacillus ha
65	20	22.5	17	11	Q9JLA7	Q9jla7 mus musculu
66	20	22.5	18	3	Q9UR73	Q9ur73 trichoderma
67	20	22.5	18	4	Q9UCF9	Q9ucf9 homo sapien
68	20	22.5	18	6	O97773	O97773 cercopithec
69	20	22.5	18	6	Q7YRH7	Q7yrh7 sus scrofa
70	20	22.5	18	11	Q7TNW8	Q7tnw8 rattus norv
71	20	22.5	18	11	Q7TNW7	Q7tnw7 mus musculu
72	19.5	21.9	15	10	P83184	P83184 triticum ae
73	19	21.3	10	12	Q9Q0W9	Q9q0w9 polyomaviru
74	19	21.3	10	12	Q8JV70	Q8jv70 polyomaviru
75	19	21.3	10	12	Q9Q0W1	Q9q0w1 polyomaviru
76	19	21.3	10	12	Q8JV68	Q8jv68 polyomaviru
77	19	21.3	10	12	Q9Q0V9	Q9q0v9 polyomaviru
78	19	21.3	10	12	Q9Q0W7	Q9q0w7 polyomaviru
79	19	21.3	10	12	Q8JV66	Q8jv66 polyomaviru
80	19	21.3	10	12	Q9Q0V7	Q9q0v7 polyomaviru
81	19	21.3	10	12	Q8JV82	Q8jv82 polyomaviru
82	19	21.3	10	12	Q8JV76	Q8jv76 polyomaviru
83	19	21.3	10	12	Q8JV74	Q8jv74 polyomaviru
84	19	21.3	10	12	Q9Q0X7	Q9q0x7 polyomaviru
85	19	21.3	10	12	Q9Q0W5	Q9q0w5 polyomaviru
86	19	21.3	10	12	Q9Q0X3	Q9q0x3 polyomaviru
87	19	21.3	10	12	Q9Q0X5	Q9q0x5 polyomaviru
88	19	21.3	10	12	Q9Q0W3	Q9q0w3 polyomaviru
89	19	21.3	10	12	Q8JV80	Q8jv80 polyomaviru
90	19	21.3	10	12	Q9Q0X1	Q9q0x1 polyomaviru
91	19	21.3	10	12	Q9Q0X9	Q9q0x9 polyomaviru
92	19	21.3	10	12	Q8JV72	Q8jv72 polyomaviru
93	19	21.3	11	4	Q9C057	Q9c057 homo sapien
94	19	21.3	11	12	Q80B26	Q80b26 hepatitis b
95	19	21.3	12	2	Q9R5F7	Q9r5f7 helicobacte
96	19	21.3	13	9	Q8HA05	Q8ha05 bacteriopha
97	19	21.3	14	2	Q8RK22	Q8rk22 pseudomonas
98	19	21.3	14	2	Q47599	Q47599 escherichia
99	19	21.3	14	15	Q8JDM3	Q8jdm3 human immun
100	19	21.3	14	15	Q8JDM7	Q8jdm7 human immun

#### ALIGNMENTS

#### RESULT 1

Q9TWM9

ID Q9TWM9 PRELIMINARY; PRT; 18 AA.  
AC Q9TWM9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE NKTAG antigen (Fragment).  
OS Tetrahymena pyriformis.

OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;  
 OC Tetrahymenina; Tetrahymena.  
 OX NCBI\_TaxID=5908;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94323706; PubMed=7519359;  
 RA Leary J.H.3rd, Evans D.L., Jaso-Friedmann L.;  
 RT "Partial amino acid sequence of a novel protozoan parasite antigen  
 RT that inhibits non-specific cytotoxic cell activity.";  
 RL Scand. J. Immunol. 40:158-164(1994).  
 SQ SEQUENCE 18 AA; 2082 MW; 13BCB737B1FF92A3 CRC64;

Query Match 36.0%; Score 32; DB 5; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 LQVMMEPQGD 17  
 ||: ||||  
 Db 3 LQLPFNPQGD 12

## RESULT 2

Q7Y0I3

ID Q7Y0I3 PRELIMINARY; PRT; 17 AA.  
 AC Q7Y0I3;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Isoamylase (Fragment).  
 GN SU1.  
 OS Zea mays subsp. mays (maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4578;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. T232;  
 RA Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,  
 RA Buckler E.S. IV.;  
 RT "Dissection of maize starch production by candidate gene  
 RT association.";  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY290391; AAP45416.1; -.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1810 MW; E2913BED794C0670 CRC64;

Query Match 31.5%; Score 28; DB 10; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 1e+03;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQV 10  
 : :||| |  
 Db 8 VSSPRLLAV 17

## RESULT 3

Q8MC25

ID Q8MC25 PRELIMINARY; PRT; 16 AA.  
AC Q8MC25;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Sonneratia apetala.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Sonneratia.  
OX NCBI\_TaxID=122813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S165;  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences."  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035740; AAL14161.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
:::|::| :::::  
Db 3 IRSPEPEVKILVD 15

RESULT 4

Q8MC39

ID Q8MC39 PRELIMINARY; PRT; 16 AA.  
AC Q8MC39;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Ammannia baccifera.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Ammannia.  
OX NCBI\_TaxID=162022;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A610;  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based

RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035733; AAL14147.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|::| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 5

## Q8LVE1

ID Q8LVE1 PRELIMINARY; PRT; 16 AA.  
 AC Q8LVE1;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsaA (Fragment).  
 GN PSAA.  
 OS Punica granatum (Pomegranate).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Punica.  
 OX NCBI\_TaxID=22663;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=P728, and P745;  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035724; AAL14129.1; -.  
 DR EMBL; AY035742; AAL14165.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|::| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 6

Q8MC53

ID Q8MC53 PRELIMINARY; PRT; 16 AA.  
AC Q8MC53;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Woodfordia fruticosa.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Woodfordia.  
OX NCBI\_TaxID=141189;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W493;  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences."  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035722; AAL14125.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
:::|::| :::::  
Db 3 IRSPEPEVKILVD 15

# RESULT 7

Q8MC17

ID Q8MC17 PRELIMINARY; PRT; 16 AA.  
AC Q8MC17;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Ludwigia hyssopifolia.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Onagraceae; Ludwigia.  
OX NCBI\_TaxID=155013;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=L787;  
RA Huang Y., Shi S.;

RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035745; AAL14171.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|::| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 8

## Q8LVE2

ID Q8LVE2 PRELIMINARY; PRT; 16 AA.  
 AC Q8LVE2;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsaA (Fragment).  
 GN PSAA.  
 OS Lythrum salicaria (Purple loosestrife).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Lythrum.  
 OX NCBI\_TaxID=13129;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=L758, and 758F;  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035727; AAL14135.1; -.  
 DR EMBL; AF421495; AAM45853.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|::| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 9

Q8LVE0

ID Q8LVE0 PRELIMINARY; PRT; 16 AA.  
AC Q8LVE0;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS *Trapa maximowiczii*.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; *Trapa*.  
OX NCBI\_TaxID=162053;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=T744, and T010;  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast *rbcL* Gene, *psaA-ycf3* Spacer, and Nuclear *rDNA* Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035729; AAL14139.1; -.  
DR EMBL; AY035730; AAL14141.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
:::|::| :::::  
Db 3 IRSPEPEVKILVD 15

# RESULT 10

Q8MET2

ID Q8MET2 PRELIMINARY; PRT; 16 AA.  
AC Q8MET2;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PSI P700 apoprotein A1 (Fragment).  
GN PSAA.  
OS *Saxifraga stolonifera*.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Saxifragales; Saxifragaceae; *Saxifraga*.  
OX NCBI\_TaxID=182070;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;  
 RT "Phylogeny of the Altingiaceae based on cpDNA matK, PY-IGS and nrDNA  
 RT ITS sequences.";  
 RL Plant Syst. Evol. 230:13-24(2001).  
 DR EMBL; AF377995; AAM45512.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|::| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 11

## Q8MC45

ID Q8MC45 PRELIMINARY; PRT; 16 AA.  
 AC Q8MC45;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsaA (Fragment).  
 GN PSAA.  
 OS Decodon verticillatus (Swamp loosestrife).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Decodon.  
 OX NCBI\_TaxID=162018;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D212;  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035728; AAL14137.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|::| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 12

Q8MC21

ID Q8MC21 PRELIMINARY; PRT; 16 AA.  
AC Q8MC21;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Combretum wallichii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Combretaceae; Combretum.  
OX NCBI\_TaxID=131243;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C505;  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035743; AAL14167.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
:::|::| :::::  
Db 3 IRSPEPEVKILVD 15

# RESULT 13

Q8MC51

ID Q8MC51 PRELIMINARY; PRT; 16 AA.  
AC Q8MC51;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Cuphea lanceolata.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Cuphea.  
OX NCBI\_TaxID=3930;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C490;  
RA Huang Y., Shi S.;

RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035723; AAL14127.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|:| :::::  
 Db 3 IRSPEPEVKILVD 15

#### RESULT 14

##### Q8MC33

ID Q8MC33 PRELIMINARY; PRT; 16 AA.  
 AC Q8MC33;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsaA (Fragment).  
 GN PSAA.  
 OS Rotala indica.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Rotala.  
 OX NCBI\_TaxID=162024;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R492;  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035736; AAL14153.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|:| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 15

Q8MC19

ID Q8MC19 PRELIMINARY; PRT; 16 AA.  
AC Q8MC19;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Quisqualis indica (Rangoon creeper).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Combretaceae; Quisqualis.  
OX NCBI\_TaxID=3956;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Q379;  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035744; AAL14169.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
::|::| :::::  
Db 3 IRSPEPEVKILVD 15

# RESULT 16

Q8MC49

ID Q8MC49 PRELIMINARY; PRT; 16 AA.  
AC Q8MC49;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Pemphis acidula.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Pemphis.  
OX NCBI\_TaxID=126635;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=P630;  
RA Huang Y., Shi S.;

RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035725; AAL14131.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|:| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 17

Q8MC27

ID Q8MC27 PRELIMINARY; PRT; 16 AA.  
 AC Q8MC27;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsaA (Fragment).  
 GN PSAA.  
 OS Lagerstroemia villosa.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Lagerstroemia.  
 OX NCBI\_TaxID=162025;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=L688;  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035739; AAL14159.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|:| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 18

Q8MET0

ID Q8MET0 PRELIMINARY; PRT; 16 AA.  
AC Q8MET0;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PSI P700 apoprotein A1 (Fragment).  
GN PSAA.  
OS Cercidiphyllum japonicum (Katsura tree).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Saxifragales; Cercidiphyllaceae; Cercidiphyllum.  
OX NCBI\_TaxID=13413;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;  
RT "Phylogeny of the Altingiaceae based on cpDNA matK, PY-IGS and nrDNA  
RT ITS sequences.";  
RL Plant Syst. Evol. 230:13-24(2001).  
DR EMBL; AF377996; AAM45514.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;

Best Local Similarity 15.4%; Pred. No. 1.4e+03;

Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
:::|::| :::::  
Db 3 IRSPEPEVKILVD 15

# RESULT 19

Q8MC23

ID Q8MC23 PRELIMINARY; PRT; 16 AA.  
AC Q8MC23;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Sonneratia alba.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Sonneratia.  
OX NCBI\_TaxID=122812;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S482;  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal

RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035741; AAL14163.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|:| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 20

Q8MC41

ID Q8MC41 PRELIMINARY; PRT; 16 AA.  
 AC Q8MC41;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsaA (Fragment).  
 GN PSAA.  
 OS Nesaea luederitzi.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Nesaea.  
 OX NCBI\_TaxID=162020;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=N213;  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035732; AAL14145.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|:| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 21

Q8MC15

ID Q8MC15 PRELIMINARY; PRT; 16 AA.  
AC Q8MC15;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Fuchsia hybrid cultivar.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Onagraceae; Fuchsia.  
OX NCBI\_TaxID=133545;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F016;  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035746; AAL14173.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
:::|::| :::::  
Db 3 IRSPEPEVKILVD 15

#### RESULT 22

Q8MC43

ID Q8MC43 PRELIMINARY; PRT; 16 AA.  
AC Q8MC43;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Sonneratia caseolaris.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Sonneratia.  
OX NCBI\_TaxID=122814;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S435;  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal

RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035731; AAL14143.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|::| :::::  
 Db 3 IRSPEPEVKILVD 15

#### RESULT 23

Q8MC47

ID Q8MC47 PRELIMINARY; PRT; 16 AA.  
 AC Q8MC47;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsaA (Fragment).  
 GN PSAA.  
 OS Peplis portula.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Peplis.  
 OX NCBI\_TaxID=162016;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=P220;  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035726; AAL14133.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|::| :::::  
 Db 3 IRSPEPEVKILVD 15

#### RESULT 24

Q8MC37

ID Q8MC37 PRELIMINARY; PRT; 16 AA.  
AC Q8MC37;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Lawsonia inermis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Lawsonia.  
OX NCBI\_TaxID=141191;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=L494;  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences."  
RL Int. J. Plant Sci. 163:215-225(2002).  
DR EMBL; AY035734; AAL14149.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
:::|::| :::::  
Db 3 IRSPEPEVKILVD 15

#### RESULT 25

Q8MC29

ID Q8MC29 PRELIMINARY; PRT; 16 AA.  
AC Q8MC29;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Duabanga grandiflora.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Duabanga.  
OX NCBI\_TaxID=122808;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D441;  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal

RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035738; AAL14157.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|:| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 26

Q8MC31

ID Q8MC31 PRELIMINARY; PRT; 16 AA.  
 AC Q8MC31;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsaA (Fragment).  
 GN PSAA.  
 OS Lagerstroemia speciosa.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Lythraceae; Lagerstroemia.  
 OX NCBI\_TaxID=122810;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=L477;  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035737; AAL14155.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
 Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
 :::|:| :::::  
 Db 3 IRSPEPEVKILVD 15

# RESULT 27

Q8MES8

ID Q8MES8 PRELIMINARY; PRT; 16 AA.  
AC Q8MES8;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PSI P700 apoprotein A1 (Fragment).  
GN PSAA.  
OS Daphniphyllum calycinum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Saxifragales; Daphniphyllaceae; Daphniphyllum.  
OX NCBI\_TaxID=182071;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;  
RT "Phylogeny of the Altingiaceae based on cpDNA matK, PY-IGS and nrDNA  
RT ITS sequences.";  
RL Plant Syst. Evol. 230:13-24(2001).  
DR EMBL; AF377997; AAM45516.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
:::|::| :::::  
Db 3 IRSPEPEVKILVD 15

# RESULT 28

Q8MC35

ID Q8MC35 PRELIMINARY; PRT; 16 AA.  
AC Q8MC35;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsaA (Fragment).  
GN PSAA.  
OS Heimia myrtifolia.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC Myrtales; Lythraceae; Heimia.  
OX NCBI\_TaxID=135798;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H491;  
RA Huang Y., Shi S.;  
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
RT Transcribed Spacer (ITS) Sequences.";  
RL Int. J. Plant Sci. 163:215-225(2002).

DR EMBL; AY035735; AAL14151.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA..  
KW Chloroplast.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 16;  
Best Local Similarity 15.4%; Pred. No. 1.4e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
:::|:| :::::  
Db 3 IRSPEPEVKILVD 15

#### RESULT 29

Q9XQN9

ID Q9XQN9 PRELIMINARY; PRT; 17 AA.  
AC Q9XQN9;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Photosystem I P700 chlorophyll (Fragment).  
GN PSAA.  
OS Sinapis alba (White mustard) (Brassica hirta).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Sinapis.  
OX NCBI\_TaxID=3728;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cotyledon;  
RX MEDLINE=20136375; PubMed=10672444;  
RA Summer H., Pfannschmidt T., Link G.;  
RT "Transcripts and sequence elements suggest differential promoter usage  
RT within the ycf3-psaAB gene cluster on mustard (Sinapis alba L.)  
RT chloroplast DNA.";  
RL Curr. Genet. 37:45-52(2000).  
DR EMBL; AJ242660; CAB45538.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 2008 MW; 99517FE691B89355 CRC64;

Query Match 30.3%; Score 27; DB 8; Length 17;  
Best Local Similarity 15.4%; Pred. No. 1.5e+03;  
Matches 2; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13  
:::|:| :::::  
Db 3 IRSPEPEVKILVD 15

#### RESULT 30

Q90XE2

ID Q90XE2 PRELIMINARY; PRT; 17 AA.

AC Q90XE2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Transforming growth factor beta 4 (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pan H.J., Halper J.;  
 RT "5' end sequence of chicken transforming growth factor beta 4.";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF395834; AAL05481.1; -.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1721 MW; 5080B3551E71BD63 CRC64;

Query Match 29.2%; Score 26; DB 13; Length 17;  
 Best Local Similarity 44.4%; Pred. No. 2.1e+03;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQPLLQVMM 12  
 | ||| :::  
 Db 3 PSPLLALLL 11

#### RESULT 31

##### Q9UCH1

ID Q9UCH1 PRELIMINARY; PRT; 16 AA.  
 AC Q9UCH1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE LIPOAMIDASE (EC 3.1.1.13) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93228634; PubMed=8471055;  
 RA Hui D.Y., Hayakawa K., Oizumi J.;  
 RT "Lipoamidase activity in normal and mutagenized pancreatic cholesterol  
 RT esterase (bile salt-stimulated lipase).";  
 RL Biochem. J. 291:65-69(1993).  
 DR GO; GO:0004771; F:sterol esterase activity; IEA.  
 SQ SEQUENCE 16 AA; 1844 MW; 147321FA60374B3C CRC64;

Query Match 28.1%; Score 25; DB 4; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQP 6  
 | : |||  
 Db 3 LENPQP 8

# RESULT 32

Q9TRB4

ID Q9TRB4 PRELIMINARY; PRT; 16 AA.  
AC Q9TRB4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE ATP-dependent 20 S proteasome activator (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94342244; PubMed=8063704;  
RA DeMartino G.N., Moomaw C.R., Zagnitko O.P., Proske R.J., Chu-Ping M.,  
RA Afendis S.J., Swaffield J.C., Slaughter C.A.;  
RT "PA700, an ATP-dependent activator of the 20 S proteasome, is an  
RT ATPase containing multiple members of a nucleotide-binding protein  
RT family.";  
RL J. Biol. Chem. 269:20878-20884(1994).  
SQ SEQUENCE 16 AA; 1878 MW; F70F74211EE26EDE CRC64;

Query Match 28.1%; Score 25; DB 6; Length 16;  
Best Local Similarity 36.4%; Pred. No. 2.9e+03;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 PQPLLQVMMEP 14  
|:| |: |  
Db 4 PEPNFQLLDNP 14

# RESULT 33

Q9APT4

ID Q9APT4 PRELIMINARY; PRT; 17 AA.  
AC Q9APT4;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21142509; PubMed=11208781;  
RA Liang X., Pham X.Q.T., Olson M.V., Lory S.;  
RT "Identification of a Genomic Island Present in the Majority of  
RT Pathogenic Isolates of Pseudomonas aeruginosa.";  
RL J. Bacteriol. 183:843-853(2001).  
DR EMBL; AF241171; AAK01539.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 17 AA; 1954 MW; 68FDF0471E399969 CRC64;

Query Match 28.1%; Score 25; DB 2; Length 17;  
Best Local Similarity 36.4%; Pred. No. 3.1e+03;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 PQPLLQVMMEP 14  
| | : : : |  
Db 3 PWELVDALLEP 13

RESULT 34

Q9R5F6

ID Q9R5F6 PRELIMINARY; PRT; 18 AA.  
AC Q9R5F6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Urease small subunit (Fragment).  
OS Helicobacter mustelae.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=217;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93084378; PubMed=1452359;  
RA Turbett G.R., Hoj P.B., Horne R., Mee B.J.;  
RT "Purification and characterization of the urease enzymes of  
RT Helicobacter species from humans and animals.";  
RL Infect. Immun. 60:5259-5266(1992).  
DR PIR; F49215; F49215.  
DR GO; GO:0016151; F:nickel ion binding; IEA.  
DR GO; GO:0009039; F:urease activity; IEA.  
DR GO; GO:0006807; P:nitrogen metabolism; IEA.  
DR InterPro; IPR002026; Urease\_gamma.  
DR Pfam; PF00547; urease\_gamma; 1.  
SQ SEQUENCE 18 AA; 2060 MW; 29C8E0AB77E21805 CRC64;

Query Match 28.1%; Score 25; DB 2; Length 18;  
Best Local Similarity 33.3%; Pred. No. 3.3e+03;  
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TPQPLLQVMMEPQGD 17  
| | : | : : | : | :  
Db 2 TPKELDKMMLHYAGE 16

RESULT 35

Q44237

ID Q44237 PRELIMINARY; PRT; 11 AA.  
AC Q44237;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Glutamine synthetase (Fragment).  
GN GLNA.  
OS Anabaena sp. (strain PCC 7120).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

OX NCBI\_TaxID=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PCC 7120;  
 RA Warner L.E., Ligon P.J., Stahel A.W., Curtis S.E.;  
 RT "The apcF gene of Anabaena sp. strain PCC 7120 is regulated by  
 RT nitrogen and the apcF and glnA promoters overlap.";  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PCC 7120;  
 RA Scappino L.A.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; U21853; AAA65652.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1316 MW; 2000580E32CB06C7 CRC64;

Query Match 25.8%; Score 23; DB 2; Length 11;  
 Best Local Similarity 44.4%; Pred. No. 4.3e+03;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQ 9  
 : ||| :|:  
 Db 1 MTTPQEVVK 9

# RESULT 36

Q9UEE2

ID Q9UEE2 PRELIMINARY; PRT; 13 AA.  
 AC Q9UEE2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE ERGB transcription factor (Fragment).  
 GN FLI1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Obata K., Hiraga H., Nojima T., Yoshida M.C., Abe S.;  
 RT "Molecular analysis on the breakpoint region of a t(11:22)  
 RT translocation in Ewing's sarcoma.";  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB012625; BAA32806.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1541 MW; 2C677798CB566AB7 CRC64;

Query Match 25.8%; Score 23; DB 4; Length 13;  
 Best Local Similarity 80.0%; Pred. No. 5.1e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QTPQP 6  
 | |||  
 Db 2 QRPQP 6

RESULT 37

Q96RT5

ID Q96RT5 PRELIMINARY; PRT; 16 AA.  
 AC Q96RT5;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Tuberous sclerosis 1 (Fragment).  
 GN TSC1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Fang L., Wu Z.Y., Wang N., MuRong S.X., Lin M.T., Chao D.R.,  
 RA Fang Z.M.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF274227; AAK60414.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1826 MW; 895C250451E3BBEE CRC64;

Query Match 25.8%; Score 23; DB 4; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 6.3e+03;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQV 10  
 | || ||:  
 Db 7 LNTPGQLRL 16

RESULT 38

Q84RM4

ID Q84RM4 PRELIMINARY; PRT; 16 AA.  
 AC Q84RM4;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Dehydrin-like protein Dh2 (Fragment).  
 OS Boea crassifolia.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiids; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae; Boea.  
 OX NCBI\_TaxID=104990;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shen Y., Lin Z.;  
 RT "Isolation and structural analysis of a drought-stressed dehydrin-like  
 RT gene BcDh2 promoter from Boea crassifolia."  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY243044; AA086689.1; -.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1887 MW; 399D10A6E3E2ED3E CRC64;

Query Match 25.8%; Score 23; DB 10; Length 16;  
Best Local Similarity 66.7%; Pred. No. 6.3e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 MEPQGD 17  
||| |:  
Db 1 MEPYGN 6

RESULT 39

Q7X3X0

ID Q7X3X0 PRELIMINARY; PRT; 17 AA.  
AC Q7X3X0;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative histidine kinase (Fragment).  
GN OSAA.  
OS Streptomyces lividans.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1916;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1326;  
RA Bishop A., Fielding S., Dyson P., Herron P.;  
RT "Concerted mutagenesis of a streptomycete genome: identification of a  
RT novel response regulator involved in osmoadaptation required for  
RT differentiation and regulation of antibiotic production.";  
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1326;  
RA Herron P.R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AJ565873; CAD92482.1; -.  
KW Kinase.  
FT NON\_TER 1 1  
SQ SEQUENCE 17 AA; 2127 MW; AEA57E24A45AD792 CRC64;

Query Match 25.8%; Score 23; DB 2; Length 17;  
Best Local Similarity 50.0%; Pred. No. 6.7e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 PQPLLQVMME 13  
| ||| :  
Db 3 PDHLLTVMQQ 12

RESULT 40

Q30216

ID Q30216 PRELIMINARY; PRT; 18 AA.  
AC Q30216;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Human leukocyte antigen alpha chain (Fragment).

GN HLA DQA1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95064785; PubMed=7974465;  
 RA Fogdell A., Olerup O.;  
 RT "The DQA1\*0104 allele is carried by DRB1\*1001- and DRB1\*1401-positive  
 RT haplotypes in Caucasians, Africans and Orientals.";  
 RL Tissue Antigens 44:19-24(1994).  
 DR EMBL; S75685; AAB32621.1; -.  
 DR PIR; I59649; I59649.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 18 AA; 1708 MW; 097492525C2252FC CRC64;

Query Match 25.8%; Score 23; DB 7; Length 18;  
 Best Local Similarity 55.6%; Pred. No. 7.1e+03;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 LQVMMEPQG 16  
 | ||||  
 Db 5 LTTMMSPCG 13

#### RESULT 41

Q8CG32

ID Q8CG32 PRELIMINARY; PRT; 12 AA.  
 AC Q8CG32;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE L-histidine decarboxylase (Fragment).  
 GN HDC.  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96198284; PubMed=8928792;  
 RA Hocker M., Zhang Z., Fenstermacher D.A., Tagerud S., Chulak M.,  
 RA Joseph D., Wang T.C.;  
 RT "Rat histidine decarboxylase promoter is regulated by gastrin through  
 RT a protein kinase C pathway.";  
 RL Am. J. Physiol. 270:G619-G633(1996).  
 DR EMBL; S83368; AAN86715.1; -.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1515 MW; 8783853D28FB5B05 CRC64;

Query Match 24.7%; Score 22; DB 11; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MMEP 14  
 ||||

Db 1 MMEP 4

RESULT 42

O88176

ID O88176 PRELIMINARY; PRT; 13 AA.  
AC O88176;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Neural cell adhesion molecule (Fragment).  
GN NCAM1 OR NCAM.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb-c; TISSUE=Liver;  
RX MEDLINE=98250618; PubMed=9582442;  
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;  
RT "A cis-acting regulatory element that affects the alternative splicing  
RT of a muscle-specific exon in the mouse NCAM gene."  
RL Biochim. Biophys. Acta 1397:305-315(1998).  
DR EMBL; AB001873; BAA31275.1; -.  
DR MGD; MGI:97281; Ncam1.  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 24.7%; Score 22; DB 11; Length 13;  
Best Local Similarity 66.7%; Pred. No. 7.4e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQPLLQ 9

| |:||

Db 3 PLPVLQ 8

RESULT 43

Q8CIW3

ID Q8CIW3 PRELIMINARY; PRT; 13 AA.  
AC Q8CIW3;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE MORF4-related protein (Fragment).  
GN MORF4L1 OR TEX189.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvEv;  
RX MEDLINE=22220132; PubMed=12234683;  
RA Tominaga K., Pereira-Smith O.;

RT "The genomic organization, promoter position and expression profile of  
 RT the mouse MRG15 gene."  
 RL Gene 294:215-215(2002).  
 DR EMBL; AY072694; AAL67900.1; -.  
 DR MGD; MGI:1096551; Morf411.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1544 MW; 9B0B3B837D5A276A CRC64;

Query Match 24.7%; Score 22; DB 11; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 7.4e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QTPQPLLQ 9  
 | | : | |  
 Db 5 QDPKPKFQ 12

#### RESULT 44

Q9NNZ2

ID Q9NNZ2 PRELIMINARY; PRT; 16 AA.  
 AC Q9NNZ2;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Integrin alpha-2 subunit (Fragment).  
 GN ITGA2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98421383; PubMed=9746778;  
 RA Kritzik M., Savage B., Nugent D.J., Santoso S., Ruggeri Z.M.,  
 RA Kunicki T.J.;  
 RT "Nucleotide polymorphisms in the alpha2 gene define multiple alleles  
 RT that are associated with differences in platelet alpha2 beta1  
 RT density.";  
 RL Blood 92:2382-2388(1998).  
 DR EMBL; AF062039; AAF77577.1; -.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1635 MW; F6A5FC64F83370A9 CRC64;

Query Match 24.7%; Score 22; DB 4; Length 16;  
 Best Local Similarity 71.4%; Pred. No. 9.1e+03;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQPLLQV 10  
 | | | | |  
 Db 10 PLPLLLV 16

#### RESULT 45

Q81CS8

ID Q81CS8 PRELIMINARY; PRT; 18 AA.  
 AC Q81CS8;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE ThiJ/PfpI family protein.  
 GN BC2668.  
 OS *Bacillus cereus* (strain ATCC 14579 / DSM 31).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.  
 OX NCBI\_TaxID=226900;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22608415; PubMed=12721630;  
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,  
 RA Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,  
 RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,  
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,  
 RA Overbeek R., Kyrpides N.;  
 RT "Genome sequence of *Bacillus cereus* and comparative analysis with  
 RT *Bacillus anthracis*.";  
 RL Nature 423:87-91(2003).  
 DR EMBL; AE017006; AAP09624.1; -.  
 KW Complete proteome.  
 SQ SEQUENCE 18 AA; 2008 MW; 33C208493C06B6AE CRC64;

Query Match 24.7%; Score 22; DB 16; Length 18;  
 Best Local Similarity 57.1%; Pred. No. 1e+04;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPL 7  
 | : | | :  
 Db 6 LETVQPV 12

#### RESULT 46

Q9T2Y3

ID Q9T2Y3 PRELIMINARY; PRT; 8 AA.  
 AC Q9T2Y3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE RBCL protein (Fragment).  
 GN RBCL.  
 OS *Begonia formosana*.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Cucurbitales; Begoniaceae; *Begonia*.  
 OX NCBI\_TaxID=80370;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chiang T.Y.;  
 RT "Sequence announcement: rbcL promotor gene in *Begonia formosana*.";  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AJ009599; CAB52123.1; -.  
 DR EMBL; AJ009598; CAB52121.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 907 MW; FA21AAB1B6C775B6 CRC64;

Query Match 23.6%; Score 21; DB 8; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 MEPQGD 17  
| | | |  
Db 1 MSPQTD 6

RESULT 47

Q7TSC5

ID Q7TSC5 PRELIMINARY; PRT; 10 AA.  
AC Q7TSC5;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Phosphorylase kinase (EC 2.7.1.38) (Fragment).  
GN PHKA1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb/C; TISSUE=Skeletal muscle;  
RX MEDLINE=94043107; PubMed=8226841;  
RA Wullrich A., Hamacher C., Schneider A., Kilimann M.W.;  
RT "The multiphosphorylation domain of the phosphorylase kinase alpha M  
RT alpha L subunits is a hotspot of differential mRNA processing and of  
RT molecular evolution.";  
RL J. Biol. Chem. 268:23208-23214(1993).  
DR EMBL; X73876; CAD92255.1; -.  
KW Kinase; Transferase.  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1192 MW; 5D18211685A2D5B7 CRC64;

Query Match 23.6%; Score 21; DB 11; Length 10;  
Best Local Similarity 62.5%; Pred. No. 8.3e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 LQVMMEPQ 15  
| | | |  
Db 3 LSVSMESQ 10

RESULT 48

Q9X637

ID Q9X637 PRELIMINARY; PRT; 15 AA.  
AC Q9X637;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE MerT (Fragment).  
GN MERT.  
OS Klebsiella oxytoca.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=571;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=509H;  
 RX MEDLINE=97208220; PubMed=9055422;  
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;  
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative  
 RT bacteria isolated from the fecal flora of primates.";  
 RL Appl. Environ. Microbiol. 63:1066-1076(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=509H;  
 RX MEDLINE=98027386; PubMed=9361435;  
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "Association of mercury resistance with antibiotic resistance in the  
 RT gram-negative fecal bacteria of primates.";  
 RL Appl. Environ. Microbiol. 63:4494-4503(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=509H;  
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "15-bp tandem repeats occur at a sharp transition in gc content in the  
 RT mer operon.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF131272; AAD37141.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0015097; F:mercury ion transporter activity; IEA.  
 DR GO; GO:0015694; P:mercury ion transport; IEA.  
 DR InterPro; IPR003457; Transprt\_MerT.  
 DR Pfam; PF02411; MerT; 1.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 23.6%; Score 21; DB 2; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MMEPQ 15  
 | |||  
 Db 1 MSEPQ 5

# RESULT 49

Q9X635

ID Q9X635 PRELIMINARY; PRT; 15 AA.  
 AC Q9X635;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE MerT (Fragment).  
 GN MERT.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=390;  
 RX MEDLINE=97208220; PubMed=9055422;  
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;  
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative  
 RT bacteria isolated from the fecal flora of primates.";  
 RL Appl. Environ. Microbiol. 63:1066-1076(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=390;  
 RX MEDLINE=98027386; PubMed=9361435;  
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "Association of mercury resistance with antibiotic resistance in the  
 RT gram-negative fecal bacteria of primates.";  
 RL Appl. Environ. Microbiol. 63:4494-4503(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=390;  
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "15-bp tandem repeats occur at a sharp transition in gc content in the  
 RT mer operon.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF131271; AAD37139.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0015097; F:mercury ion transporter activity; IEA.  
 DR GO; GO:0015694; P:mercury ion transport; IEA.  
 DR InterPro; IPR003457; Transprt\_MerT.  
 DR Pfam; PF02411; MerT; 1.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 23.6%; Score 21; DB 2; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MMEPQ 15  
 | |||  
 Db 1 MSEPQ 5

# RESULT 50

Q9UQS4

ID Q9UQS4 PRELIMINARY; PRT; 16 AA.  
 AC Q9UQS4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Glycoprotein Ib alpha variant D (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92250564; PubMed=1577776;  
 RA Lopez J.A., Ludwig E.H., McCarthy B.J.;

RT "Polymorphism of human glycoprotein Ib alpha results from a variable  
RT number of tandem repeats of a 13-amino acid sequence in the mucin-like  
RT macroglycopeptide region. Structure/function implications.";  
RL J. Biol. Chem. 267:10055-10061(1992).  
DR EMBL; S34436; AAB22152.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 16 AA; 1638 MW; 81472B42262EF630 CRC64;

Query Match 23.6%; Score 21; DB 4; Length 16;  
Best Local Similarity 75.0%; Pred. No. 1.3e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPQP 6  
||:  
Db 12 TPEP 15

Search completed: July 4, 2004, 04:45:26  
Job time : 32.9254 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:26 ; Search time 5.83582 Seconds  
(without alignments)  
151.683 Million cell updates/sec

Title: US-09-641-802-2  
Perfect score: 89  
Sequence: 1 LQTPQPLLQVMMEPQGD 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 952

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score					
1	25	28.1	18	1	CPAX_BOVIN	P22779 bos taurus
2	23	25.8	15	1	PSAO_CUCSA	P42052 cucumis sat
3	22	24.7	14	1	TAT_HV1W2	P12509 human immun
4	22	24.7	14	1	TAT_HV1Z8	P12511 human immun
5	22	24.7	16	1	CFAB_BOVIN	P81187 bos taurus
6	21	23.6	10	1	FAR6_PANRE	P82660 panagrellus
7	21	23.6	16	1	FOR1_MYRGU	P81438 myrmecia gu
8	21	23.6	18	1	LCTN_LAMGL	P83315 lama glama
9	20	22.5	11	1	RANC_RANPI	P08951 rana pipien
10	20	22.5	16	1	FOR2_MYRGU	P81437 myrmecia gu
11	20	22.5	16	1	ODO2_BOVIN	P11179 bos taurus
12	19.5	21.9	14	1	UC34_MAIZE	P80640 zea mays (m
13	19	21.3	9	1	AL10_CARMA	P81813 carcinus ma
14	19	21.3	9	1	FAR9_ASCSU	P43172 ascaris suu
15	19	21.3	12	1	FIF1_SARBU	P83349 sarcophaga
16	19	21.3	15	1	UC29_MAIZE	P80635 zea mays (m
17	19	21.3	17	1	YALA_TRYBB	P17961 trypanosoma

18	18	20.2	9	1	OXYT_RAJCL	P42994	raja clavat
19	18	20.2	11	1	CEP1_ACHFU	P22790	achatina fu
20	18	20.2	13	1	GER1_HORVU	P28525	hordeum vul
21	18	20.2	13	1	GER2_HORVU	P28526	hordeum vul
22	17	19.1	8	1	WP1_PERAT	P83195	perkinsus a
23	17	19.1	9	1	FAR1_CALVO	P41856	calliphora
24	17	19.1	9	1	MGMT_BOVIN	P29177	bos taurus
25	17	19.1	9	1	RT33_BOVIN	P82926	bos taurus
26	17	19.1	10	1	RT02_BOVIN	P82923	bos taurus
27	17	19.1	11	1	HS70_PINPS	P81672	pinus pinas
28	17	19.1	11	1	TKNA_GADMO	P28498	gadus morhu
29	17	19.1	12	1	TKN1_KASMA	P08613	kassina mac
30	17	19.1	13	1	ACT7_SOYBN	P15987	glycine max
31	17	19.1	13	1	LPAA_PORGI	P81411	porphyromon
32	17	19.1	14	1	ECDC_LYMDI	P80940	lymantria d
33	17	19.1	15	1	ARCA_STRP5	P58827	streptococc
34	17	19.1	15	1	URE2_MORMO	P17338	morganella
35	17	19.1	15	1	VORA_METTM	P80907	methanobact
36	17	19.1	17	1	ACT6_SOYBN	P15986	glycine max
37	17	19.1	17	1	B29K_PORGI	P81784	porphyromon
38	17	19.1	17	1	PC24_BRANA	P81097	brassica na
39	17	19.1	17	1	PSBL_SYNVU	P12241	synechococc
40	17	19.1	18	1	HEX_ADECU	P35985	canine aden
41	16	18.0	8	1	NPMB_BOVIN	P15507	bos taurus
42	16	18.0	8	1	UF06_MOUSE	P38644	mus musculu
43	16	18.0	10	1	TKN_PHYBI	P08610	phyllomedus
44	16	18.0	10	1	UPA2_HUMAN	P30088	homo sapien
45	16	18.0	11	1	BPP3_BOTIN	P30423	bothrops in
46	16	18.0	12	1	NUDM_CANFA	P54713	canis famil
47	16	18.0	12	1	TM2A_METMA	P80652	methanosarc
48	16	18.0	13	1	CRBL_ICASP	P17237	icaria sp.
49	16	18.0	14	1	UN37_CLOPA	P81358	clostridium
50	16	18.0	15	1	COXI_THUOB	P80978	thunnus obe
51	16	18.0	15	1	CYSK_CLOPA	P81340	clostridium
52	16	18.0	15	1	ECDA_LYMDI	P80938	lymantria d
53	16	18.0	15	1	FKB7_PINPS	P81104	pinus pinas
54	16	18.0	15	1	SODM_STRGR	P80733	streptomyce
55	16	18.0	16	1	BRB_BASAL	P83187	basella alb
56	16	18.0	16	1	UPAB_HUMAN	P31935	homo sapien
57	16	18.0	17	1	A45K_MYCBO	P80069	mycobacteri
58	16	18.0	17	1	APID_BOMPA	P81464	bombus pasc
59	16	18.0	17	1	EFG_THEAQ	Q01697	thermus aqu
60	16	18.0	18	1	CXA1_CONER	P50982	conus ermin
61	16	18.0	18	1	HEMH_THETS	P80155	theromyzon
62	15	16.9	7	1	CARP_MYTED	P10420	mytilus edu
63	15	16.9	7	1	UF04_MOUSE	P38642	mus musculu
64	15	16.9	8	1	UH09_RAT	P56575	rattus norv
65	15	16.9	9	1	SAP_STOVA	P24047	stomopneute
66	15	16.9	10	1	BPP2_BOTJA	P01022	bothrops ja
67	15	16.9	10	1	PNEU_HUMAN	P22103	homo sapien
68	15	16.9	10	1	PNEU_RAT	P21996	rattus norv
69	15	16.9	11	1	BPP4_BOTIN	P30424	bothrops in
70	15	16.9	11	1	BPPB_AGKHA	P01021	agkistrodon
71	15	16.9	11	1	TKNA_CHICK	P19850	gallus gall
72	15	16.9	11	1	TKNA_HORSE	P01290	equus cabal
73	15	16.9	11	1	TKNA_ONCMY	P28499	oncorhynch
74	15	16.9	11	1	TKNA_SCYCA	P41333	scyliorhinu

75	15	16.9	13	1	BP37_LEUMA	P81754 leucophaea
76	15	16.9	13	1	BPP1_BOTJA	P01020 bothrops ja
77	15	16.9	13	1	EI21_LITRU	P82097 litoria rub
78	15	16.9	13	1	TA13_TREME	P01370 tremella me
79	15	16.9	13	1	TY13_PHYRO	P04096 phyllomedus
80	15	16.9	14	1	KLPS_SCARA	P58396 scaptocosa
81	15	16.9	14	1	MAST_POLJA	P01517 polistes ja
82	15	16.9	15	1	IRBP_CRISP	P12665 cricetidae
83	15	16.9	15	1	LEC3_PSOSC	P22583 psophocarpu
84	15	16.9	15	1	MAOX_CHICK	Q92060 gallus gall
85	15	16.9	15	1	MK1_PALPR	P80408 palomena pr
86	15	16.9	15	1	MK2A_PALPR	P80409 palomena pr
87	15	16.9	15	1	PRP_MYCBO	P80149 mycobacteri
88	15	16.9	15	1	UC30_MAIZE	P80636 zea mays (m
89	15	16.9	15	1	UN01_PINPS	P81106 pinus pinas
90	15	16.9	15	1	UP02_METAN	P83439 metarhizium
91	15	16.9	16	1	IBP4_PIG	P24854 sus scrofa
92	15	16.9	16	1	MK2B_PALPR	P80410 palomena pr
93	15	16.9	16	1	MK3_PALPR	P80411 palomena pr
94	15	16.9	16	1	SAL3_ONCMY	P82240 oncorhynchu
95	15	16.9	17	1	PH4_PERAM	P82697 periplaneta
96	15	16.9	18	1	FIBA_CAMDR	P14444 camelus dro
97	15	16.9	18	1	FIBA_LAMGL	P14454 lama glama
98	15	16.9	18	1	NPMA_BOVIN	P15506 bos taurus
99	14.5	16.3	14	1	MARI_ALTSP	P29399 alteromonas
100	14	15.7	7	1	EI05_LITRU	P82101 litoria rub

#### ALIGNMENTS

##### RESULT 1

CPAX\_BOVIN

ID CPAX\_BOVIN STANDARD; PRT; 18 AA.

AC P22779;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Cytochrome P450 2A (OLF2) (Olfactive) (P52) (EC 1.14.14.1) (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE.

RX MEDLINE=91027757; PubMed=2121272;

RA Lazard D., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;

RT "Identification and biochemical analysis of novel olfactory-specific  
cytochrome P-450IIA and UDP-glucuronosyl transferase.";

RL Biochemistry 29:7433-7440(1990).

CC -!- FUNCTION: Cytochromes P450 are a group of heme-thiolate  
monooxygenases. In liver microsomes, this enzyme is involved in an  
NADPH-dependent electron transport pathway. It oxidizes a variety  
of structurally unrelated compounds, including steroids, fatty  
acids, and xenobiotics.

CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +

CC oxidized flavoprotein + H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.  
 CC -!- SIMILARITY: Belongs to the cytochrome P450 family.  
 DR PIR; A35704; A35704.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; PARTIAL.  
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
 KW Microsome; Endoplasmic reticulum; Olfaction.  
 FT NON\_TER 1 1  
 FT VARIANT 6 6 G -> D.  
 FT VARIANT 11 11 A -> E.  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 2058 MW; F80746F76CCD77FF CRC64;

Query Match 28.1%; Score 25; DB 1; Length 18;  
 Best Local Similarity 46.2%; Pred. No. 4.4e+02;  
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 PQPLLQVMMEPQG 16  
 | | | | |  
 Db 5 PGPQQQAFKELQG 17

#### RESULT 2

PSAO\_CUCSA  
 ID PSAO\_CUCSA STANDARD; PRT; 15 AA.  
 AC P42052;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Photosystem 1 reaction centre subunit 8 (Photosystem I 17.5 kDa protein) (Fragment).  
 GN PSAM.  
 OS Cucumis sativus (Cucumber).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
 OX NCBI\_TaxID=3659;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cotyledon;  
 RX MEDLINE=91355209; PubMed=1883835;  
 RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;  
 RT "Characterization of genes that encode subunits of cucumber PS I complex by N-terminal sequencing."  
 RL Biochim. Biophys. Acta 1059:141-148(1991).  
 CC -!- FUNCTION: Essential for the activity of NADP photoreduction.  
 DR PIR; E56819; E56819.  
 KW Photosystem I; Photosynthesis; Chloroplast; Thylakoid; Membrane.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1714 MW; CA0BF5DAD403D9F4 CRC64;

Query Match 25.8%; Score 23; DB 1; Length 15;  
 Best Local Similarity 30.8%; Pred. No. 7.8e+02;  
 Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13

Db                   :| | ||: :  
1 IQADXPTFQVIQD 13

RESULT 3

TAT\_HV1W2

ID TAT\_HV1W2           STANDARD;       PRT;     14 AA.  
AC P12509;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE TAT protein (Transactivating regulatory protein) (Fragment).  
GN TAT.  
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11705;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86235450; PubMed=3012778;  
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,  
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;  
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or  
RT at risk for AIDS.";  
RL Science 232:1548-1553(1986).  
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the  
CC trans-activating responsive sequence (TAR) RNA element and  
CC activates transcription initiation and/or elongation from the LTR  
CC promoter.  
CC -!- SUBUNIT: Binds cyclin T1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.  
CC -!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM  
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO  
CC WAS PERINATALLY INFECTED BY HER MOTHER.  
CC -----  
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CC -----  
DR EMBL; M12507; AAB12991.1; -.  
DR HIV; M12507; TAT\$WMJ2.  
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;  
KW AIDS.  
FT NON\_TER           1       1  
SQ SEQUENCE     14 AA;   1467 MW;   37CC737BFEF67AA8 CRC64;

Query Match                   24.7%;   Score 22;   DB 1;   Length 14;  
Best Local Similarity       60.0%;   Pred. No. 1.1e+03;  
Matches       3;   Conservative   2;   Mismatches   0;   Indels       0;   Gaps       0;

Qy                   13 EPQGD 17

:|:|

Db                   4 QPRGD 8

# RESULT 4

TAT\_HV1Z8

ID TAT\_HV1Z8 STANDARD; PRT; 14 AA.  
AC P12511;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE TAT protein (Transactivating regulatory protein) (Fragment).  
GN TAT.  
OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11681;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88281278; PubMed=3395517;  
RA Yourno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,  
RA Gallo R.C.;  
RT "Nucleotide sequence analysis of the env gene of a new Zairian  
RT isolate of HIV-1.";  
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).  
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the  
CC trans-activating responsive sequence (TAR) RNA element and  
CC activates transcription initiation and/or elongation from the LTR  
CC promoter.  
CC -!- SUBUNIT: Binds cyclin T1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.  
CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD  
CC ZAIREAN MALE.  
CC -----  
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CC -----  
DR EMBL; J03653; AAA44685.1; -.  
DR HIV; J03653; TAT\$JY1.  
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;  
KW AIDS.  
FT NON\_TER 1 1  
SQ SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;

Query Match 24.7%; Score 22; DB 1; Length 14;  
Best Local Similarity 60.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPQGD 17  
:|:|  
Db 4 QPRGD 8

# RESULT 5

CFAB\_BOVIN

ID CFAB\_BOVIN STANDARD; PRT; 16 AA.

AC P81187;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Complement factor B (EC 3.4.21.47) (C3/C5 convertase) (EC-VMFB)  
 DE (Fragment).  
 GN BF.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Blood;  
 RX MEDLINE=97428195; PubMed=9281322;  
 RA Cai G., Satoh T., Hoshi H.;  
 RT "Isolation from fetal bovine serum of a fragment b of complement  
 RT factor B-like protein improving a long-term survival of human  
 RT endothelial cells.";  
 RL Arch. Biochem. Biophys. 345:150-155(1997).  
 CC -!- FUNCTION: Factor B which is part of the alternate pathway of the  
 CC complement system is cleaved by factor D into 2 fragments: Ba and  
 CC Bb. Bb, a serine protease, then combines with complement factor 3b  
 CC to generate the C3 or C5 convertase.  
 CC -!- CATALYTIC ACTIVITY: Cleaves C3 in the alpha-chain to yield C3a and  
 CC C3b. Cleaves C5 in the alpha-chain to yield C5a and C5b. Both  
 CC cleavages take place at the C-terminal of an arginine residue.  
 CC -!- SUBUNIT: Monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to peptidase family S1.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; PARTIAL.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; PARTIAL.  
 DR PROSITE; PS00135; TRYPSIN\_SER; PARTIAL.  
 KW Complement alternate pathway; Plasma; Hydrolase; Serine protease;  
 KW Glycoprotein; Zymogen.  
 FT CHAIN 1 >16 COMPLEMENT FACTOR B BB FRAGMENT.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1762 MW; 75FF5D7F5A6A92F0 CRC64;

Query Match 24.7%; Score 22; DB 1; Length 16;  
 Best Local Similarity 25.0%; Pred. No. 1.2e+03;  
 Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 9 QVMMEPQG 16  
 : : : : : | |  
 Db 1 KIVLDPSG 8

#### RESULT 6

##### FAR6\_PANRE

ID FAR6\_PANRE STANDARD; PRT; 10 AA.  
 AC P82660;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RP SEQUENCE, FUNCTION, AND AMIDATION.  
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
RA Maule A.G.;  
RT "Isolation, characterization and pharmacology of RMRFamide-related  
RT peptides (FaRPs) from free-living nematode, Panagrellus redivivus.";  
RL Submitted (JUL-2000) to Swiss-Prot.  
CC -!- FUNCTION: Myoactive.  
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 23.6%; Score 21; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQPLLQ 9  
||| ::  
Db 4 PQPFVR 9

# RESULT 7

## FOR1\_MYRGU

ID FOR1\_MYRGU STANDARD; PRT; 16 AA.  
AC P81438;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Formaecin 1.  
OS Myrmecia gulosa (Red bulldog ant).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Formicidae; Myrmeciinae; Myrmeciini; Myrmecia.  
OX NCBI\_TaxID=36170;  
RN [1]  
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.  
RC TISSUE=Hemolymph;  
RX MEDLINE=98165787; PubMed=9497332;  
RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;  
RT "Isolation from an ant Myrmecia gulosa of two inducible  
RT O-glycosylated proline-rich antibacterial peptides.";  
RL J. Biol. Chem. 273:6139-6143(1998).  
CC -!- FUNCTION: Antibacterial peptide. Has activity against E.coli  
CC but none against other Gram-negative bacteria and Gram-positive  
CC bacteria.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- INDUCTION: By bacterial infection.  
CC -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-  
CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.  
CC -!- SIMILARITY: TO DROSOPHILA DROSOCIN.

KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.  
FT CARBOHYD 11 11 O-LINKED (GALNAC. . .).  
SQ SEQUENCE 16 AA; 1794 MW; 80CEA3AABBC2E0AE CRC64;

Query Match 23.6%; Score 21; DB 1; Length 16;  
Best Local Similarity 66.7%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TPQPLL 8  
|||  
Db 11 TPHPRL 16

#### RESULT 8

##### LCTN\_LAMGL

ID LCTN\_LAMGL STANDARD; PRT; 18 AA.  
AC P83315;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lactophorin (Whey protein) (Fragment).  
OS Lama glama (Llama).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.  
OX NCBI\_TaxID=9844;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=20000588; PubMed=10531593;  
RA Kappeler S., Farah Z., Puhan Z.;  
RT "Alternative splicing of lactophorin mRNA from lactating mammary gland  
RT of the camel (Camelus dromedarius).";  
RL J. Dairy Sci. 82:1-10(1999).  
CC -!- SIMILARITY: Belongs to the PP3 / GlyCAM-1 family.  
DR GO; GO:0005576; C:extracellular; ISS.  
DR InterPro; IPR007906; GLYCAM-1.  
DR Pfam; PF05242; GLYCAM-1; 1.  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 2079 MW; CD59616E5B236AC6 CRC64;

Query Match 23.6%; Score 21; DB 1; Length 18;  
Best Local Similarity 36.4%; Pred. No. 2e+03;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQ 15  
:| :: |||  
Db 7 EPKDEIYMESQ 17

#### RESULT 9

##### RANC\_RANPI

ID RANC\_RANPI STANDARD; PRT; 11 AA.  
AC P08951;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ranatensin-C.  
OS Rana pipiens (Northern leopard frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8404;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=84131098; PubMed=6141890;  
 RA Nakajima T.;  
 RL Unpublished results, cited by:  
 RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;  
 RL Comp. Biochem. Physiol. 77C:99-108(1984).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin  
 CC family.  
 DR InterPro; IPR000874; Bombesin.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Amphibian defense peptide; Bombesin family; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 22.5%; Score 20; DB 1; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTPQ 5  
 :|||  
 Db 1 ZTPQ 4

#### RESULT 10

##### FOR2\_MYRGU

ID FOR2\_MYRGU STANDARD; PRT; 16 AA.  
 AC P81437;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Formaecin 2.  
 OS Myrmecia gulosa (Red bulldog ant).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Formicidae; Myrmeciinae; Myrmeciini; Myrmecia.  
 OX NCBI\_TaxID=36170;  
 RN [1]  
 RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=98165787; PubMed=9497332;  
 RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;  
 RT "Isolation from an ant Myrmecia gulosa of two inducible  
 RT O-glycosylated proline-rich antibacterial peptides."  
 RL J. Biol. Chem. 273:6139-6143(1998).  
 CC -!- FUNCTION: Antibacterial peptide. Has activity against E.coli but  
 CC none against other Gram-negative bacteria and Gram-positive  
 CC bacteria.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- INDUCTION: By bacterial infection.

CC -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-  
 CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.  
 CC -!- SIMILARITY: TO DROSOPHILA DROSOCIN.  
 KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.  
 FT CARBOHYD 11 11 O-LINKED (GALNAC. . .).  
 SQ SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;

Query Match 22.5%; Score 20; DB 1; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 2.6e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TPQPLL 8  
 || ||  
 Db 11 TPYPRL 16

# RESULT 11

## ODO2\_BOVIN

ID ODO2\_BOVIN STANDARD; PRT; 16 AA.  
 AC P11179;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Dihydrolipoamide succinyltransferase component of 2-oxoglutarate  
 DE dehydrogenase complex (EC 2.3.1.61) (E2) (Fragment).  
 GN DLST.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Kidney;  
 RX MEDLINE=88005143; PubMed=3115829;  
 RA Bradford A.P., Aitken A., Beg F., Cook K.G., Yeaman S.J.;  
 RT "Amino acid sequence surrounding the lipoic acid cofactor of bovine  
 RT kidney 2-oxoglutarate dehydrogenase complex."  
 RL FEBS Lett. 222:211-214(1987).  
 CC -!- FUNCTION: The 2-oxoglutarate dehydrogenase complex catalyzes the  
 CC overall conversion of 2-oxoglutarate to succinyl-CoA and CO(2). It  
 CC contains multiple copies of 3 enzymatic components: 2-oxoglutarate  
 CC dehydrogenase (E1), dihydrolipoamide succinyltransferase (E2) and  
 CC lipoamide dehydrogenase (E3).  
 CC -!- CATALYTIC ACTIVITY: Succinyl-CoA + dihydrolipoamide = CoA + S-  
 CC succinyl-dihydrolipoamide.  
 CC -!- COFACTOR: Contains 1 covalently bound lipoyl cofactor.  
 CC -!- PATHWAY: Tricarboxylic acid cycle.  
 CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral  
 CC symmetry.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.  
 CC -!- SIMILARITY: Contains 1 lipoyl-binding domain.  
 DR PIR; S00123; S00123.  
 DR InterPro; IPR003016; Lipoyl\_BS.  
 DR PROSITE; PS00189; LIPOYL; PARTIAL.  
 KW Tricarboxylic acid cycle; Transferase; Acyltransferase; Lipoyl;

KW Mitochondrion.  
 FT NON\_TER 1 1  
 FT BINDING 5 5 LIPOYL.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1643 MW; E34CD29B86B3239D CRC64;

Query Match 22.5%; Score 20; DB 1; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQP 6  
 :| | |  
 Db 8 VQVPSP 13

# RESULT 12

UC34\_MAIZE

ID UC34\_MAIZE STANDARD; PRT; 14 AA.  
 AC P80640;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 360)  
 DE (Fragments).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 5.7, its MW is: 41.1 kDa.  
 CC -!- CAUTION: The order of the peptides shown is uncertain.  
 DR Maize-2DPAGE; P80640; COLEOPTILE.  
 DR MaizeDB; 123965; -.  
 FT NON\_TER 1 1  
 FT NON\_CONS 8 9  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1527 MW; DC525FF7B0BE682D CRC64;

Query Match 21.9%; Score 19.5; DB 1; Length 14;  
 Best Local Similarity 54.5%; Pred. No. 2.8e+03;  
 Matches 6; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 5 QPL-LQVMMEP 14  
 :|| | | ||  
 Db 4 EPLALSVFDEP 14

# RESULT 13

## AL10\_CARMA

ID AL10\_CARMA STANDARD; PRT; 9 AA.  
 AC P81813;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 10.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidea; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.  
 CC -!- SIMILARITY: Belongs to the allatostatin family.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 963 MW; 372D79CDCB4776C7 CRC64;

Query Match 21.3%; Score 19; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PQP 6  
 |||  
 Db 2 PQP 4

## RESULT 14

## FAR9\_ASCSU

ID FAR9\_ASCSU STANDARD; PRT; 9 AA.  
 AC P43172;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE FMRFamide-like neuropeptide AF9.  
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;  
 OC Ascarididae; Ascaris.  
 OX NCBI\_TaxID=6253;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95380362; PubMed=7651904;  
 RA Cowden C., Stretton A.O.W.;  
 RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode  
 RT Ascaris suum.";  
 RL Peptides 16:491-500(1995).  
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.

KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 21.3%; Score 19; DB 1; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PQPL 7  
|:|  
Db 4 PRPL 7

#### RESULT 15

##### FIF1\_SARBU

ID FIF1\_SARBU STANDARD; PRT; 12 AA.  
AC P83349;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neb-FIRFamide 1.  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]  
RP SEQUENCE, AMIDATION, AND FUNCTION.  
RC TISSUE=CNS;  
RX MEDLINE=22342733; PubMed=12438685;  
RA Meeusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;  
RT "Identification in Drosophila melanogaster of the invertebrate G  
RT protein-coupled FMRFamide receptor."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular  
CC junctions.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 12 12 AMIDATION.  
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

Query Match 21.3%; Score 19; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PQP 6  
|||  
Db 3 PQP 5

#### RESULT 16

##### UC29\_MAIZE

ID UC29\_MAIZE STANDARD; PRT; 15 AA.  
AC P80635;

DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)  
 DE (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 4.9, its MW is: 37.6 kDa.  
 DR Maize-2DPAGE; P80635; COLEOPTILE.  
 DR MaizeDB; 123960; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;

Query Match 21.3%; Score 19; DB 1; Length 15;  
 Best Local Similarity 42.9%; Pred. No. 3.6e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQPLLQV 10  
 | ||: :  
 Db 6 PIPLVDI 12

#### RESULT 17

YALA\_TRYBB

ID YALA\_TRYBB STANDARD; PRT; 17 AA.

AC P17961;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 1.9 kDa protein in aldolase locus (ORFA).

OS Trypanosoma brucei brucei.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

OX NCBI\_TaxID=5702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=427;

RX MEDLINE=90272402; PubMed=2349093;

RA Vijayasarathy S., Ernest I., Itzhaki J., Sherman D., Mowatt M.R.,

RA Michels P.A.M., Clayton C.E.;

RT "The genes encoding fructose biphosphate aldolase in Trypanosoma

RT brucei are interspersed with unrelated genes.";

RL Nucleic Acids Res. 18:2967-2975(1990).

CC

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CC -----  
DR EMBL; X52586; CAA36821.1; -.  
DR PIR; S15064; S15064.  
KW Hypothetical protein.  
SQ SEQUENCE 17 AA; 1939 MW; 5FC2B9AF44AEF420 CRC64;

Query Match 21.3%; Score 19; DB 1; Length 17;  
Best Local Similarity 60.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QTPQP 6  
| |:  
Db 11 QLPRP 15

#### RESULT 18

##### OXYT\_RAJCL

ID OXYT\_RAJCL STANDARD; PRT; 9 AA.  
AC P42994;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Glumitocin.  
OS Raja clavata (Thornback ray).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Squalia; Hypnosqualia; Pristiorajia; Batoidea;  
OC Rajiformes; Rajidae; Raja.  
OX NCBI\_TaxID=7781;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=66123415; PubMed=5880565;  
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;  
RT "Phylogeny of neurophyophyseal peptides: isolation of a new hormone,  
RT glumitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish,  
RT the ray (Raja clavata).";  
RL Biochim. Biophys. Acta 107:393-396(1965).  
CC -!- FUNCTION: ANTIDIURETIC HORMONE.  
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.  
DR InterPro; IPR000981; Neurhyp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 984 MW; 17E9C76EB455B04B CRC64;

Query Match 20.2%; Score 18; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 PQG 16

Db                    |||  
                      7 PQG 9

RESULT 19

CEP1\_ACHFV

ID CEP1\_ACHFV            STANDARD;            PRT;       11 AA.  
AC P22790;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE Cardio-excitatory peptide-1 (ACEP-1).  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Ferussac; TISSUE=Heart atrium;  
RX MEDLINE=90211261; PubMed=2322251;  
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;  
RT "A novel cardio-excitatory peptide isolated from the atria of the  
RT African giant snail, Achatina fulica."  
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).  
CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also  
CC            excitatory actions on the penis retractor muscle, the buccal  
CC            muscle and the identified neurons controlling the buccal muscle  
CC            movement of achatina.  
CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.  
DR PIR; A34662; A34662.  
KW Hormone; Amidation.  
FT MOD\_RES            11       11            AMIDATION.  
SQ SEQUENCE       11 AA;    1305 MW;    82D6D5B9C7741365 CRC64;

Query Match                    20.2%;    Score 18;    DB 1;    Length 11;  
Best Local Similarity       100.0%;    Pred. No. 3.8e+03;  
Matches       3;    Conservative       0;    Mismatches       0;    Indels       0;    Gaps       0;

Qy                    14 PQG 16  
                      |||  
Db                    7 PQG 9

RESULT 20

GER1\_HORVU

ID GER1\_HORVU            STANDARD;            PRT;       13 AA.  
AC P28525;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Germin GS1 (Fragment).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]

RP SEQUENCE.  
 RC STRAIN=cv. CM 72; TISSUE=Root;  
 RA Hurkman W.J., Tao H.P., Tanaka C.K.;  
 RT "Germin-like polypeptides increase in barley roots during salt  
 RT stress.";  
 RL Plant Physiol. 97:366-374(1991).  
 CC -!- FUNCTION: May play a role in altering the properties of cell  
 CC walls during germinative growth.  
 CC -!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)  
 CC (By similarity).  
 CC -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSOMAL AND CELL WALL FRACTIONS.  
 CC -!- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in  
 CC the mature region, but not in the tip. Not detected in leaves.  
 CC -!- INDUCTION: Increased by salt stress in roots and decreased by salt  
 CC stress in coleoptile.  
 CC -!- PTM: Glycosylated.  
 CC -!- SIMILARITY: Belongs to the germin family.  
 DR InterPro; IPR001929; Germin.  
 DR PROSITE; PS00725; GERMIN; PARTIAL.  
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.  
 FT UNSURE 10 10  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1470 MW; 43FB588AA3B7B6D7 CRC64;

Query Match 20.2%; Score 18; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 4.5e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQPL 7  
 | ||  
 Db 3 PSPL 6

#### RESULT 21

##### GER2\_HORVU

ID GER2\_HORVU STANDARD; PRT; 13 AA.  
 AC P28526;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Germin GS2 (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. CM 72; TISSUE=Root;  
 RA Hurkman W.J., Tao H.P., Tanaka C.K.;  
 RT "Germin-like polypeptides increase in barley roots during salt  
 RT stress.";  
 RL Plant Physiol. 97:366-374(1991).  
 CC -!- FUNCTION: May play a role in altering the properties of cell walls  
 CC during germinative growth.  
 CC -!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)  
 CC (By similarity).

CC -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSOMAL AND CELL WALL FRACTIONS.  
 CC -!- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in the  
 CC mature region, but not in the tip. Not detected in leaves.  
 CC -!- INDUCTION: Increased by salt stress in roots and decreased by salt  
 CC stress in coleoptile.  
 CC -!- PTM: Glycosylated.  
 CC -!- SIMILARITY: Belongs to the germin family.  
 DR InterPro; IPR001929; Germin.  
 DR PROSITE; PS00725; GERMIN; PARTIAL.  
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.  
 FT UNSURE 10 10  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7B6D7 CRC64;

Query Match 20.2%; Score 18; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 4.5e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQPL 7  
 | |  
 Db 3 PSPL 6

#### RESULT 22

##### WP1\_PERAT

ID WP1\_PERAT STANDARD; PRT; 8 AA.  
 AC P83195;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Wall protein-1 (PWP-1) (Fragment).  
 OS Perkinsus atlanticus.  
 OC Eukaryota; Alveolata; Perkinsea; Perkinsida; Perkinsidae; Perkinsus.  
 OX NCBI\_TaxID=106964;  
 RN [1]  
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RX MEDLINE=22044350; PubMed=12049410;  
 RA Montes J.F., Durfort M., Llado A., Garcia-Valero J.;  
 RT "Characterization and immunolocalization of a main proteinaceous  
 RT component of the cell wall of the protozoan parasite Perkinsus  
 RT atlanticus.";  
 RL Parasitology 124:477-484(2002).  
 CC -!- FUNCTION: Is a major protein component of the cell wall. May play  
 CC a key role in the organization of the cell wall and in promoting  
 CC the survival of this parasite.  
 CC -!- SUBCELLULAR LOCATION: Cell wall. Disulfide-linked to other cell  
 CC wall components.  
 CC -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental  
 CC stages.  
 KW Cell wall.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 765 MW; F1787DD87B1AAB16 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 MEPQG 16  
|| :|  
Db 1 MEDEG 5

RESULT 23

FAR1\_CALVO

ID FAR1\_CALVO STANDARD; PRT; 9 AA.  
AC P41856;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CalliFMRFamide 1.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated calliFMRFamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- FUNCTION: Able to induce fluid secretion from the isolated  
CC salivary gland of Calliphora.  
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
DR PIR; A41978; A41978.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPQ 5  
|||  
Db 1 TPQ 3

RESULT 24

MGMT\_BOVIN

ID MGMT\_BOVIN STANDARD; PRT; 9 AA.  
AC P29177;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-  
DE methylguanine-DNA methyltransferase) (Fragment).  
GN MGMT.  
OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thymus;  
 RX MEDLINE=90174912; PubMed=2308822;  
 RA Rydberg B., Hall J., Karran P.;  
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA  
 RT methyltransferase.";  
 RL Nucleic Acids Res. 18:17-21(1990).  
 CC -!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically  
 CC transferring the alkyl group at the O-6 position to a cysteine  
 CC residue in the enzyme. This is a suicide reaction: the enzyme is  
 CC irreversibly inactivated.  
 CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +  
 CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein  
 CC S-methyl-L-cysteine.  
 CC -!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE  
 CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.  
 DR InterPro; IPR001497; Methyltransf\_1.  
 DR PROSITE; PS00374; MGMT; PARTIAL.  
 KW DNA repair; Transferase; Methyltransferase.  
 FT NON\_TER 1 1  
 FT ACT\_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQPLL 8  
 | |:  
 Db 2 PIPIL 6

# RESULT 25

RT33\_BOVIN  
 ID RT33\_BOVIN STANDARD; PRT; 9 AA.  
 AC P82926;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).  
 GN MRPS33.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=21276436; PubMed=11279123;  
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spemulli L.L.;

RT "The small subunit of the mammalian mitochondrial ribosome:  
 RT identification of the full complement of ribosomal proteins present.";  
 RL J. Biol. Chem. 276:19363-19374(2001).  
 CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit  
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON\_TER 1 1  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1.4e+05;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQPL 7  
 | : |||  
 Db 1 LFSEQPL 7

# RESULT 26

RT02\_BOVIN  
 ID RT02\_BOVIN STANDARD; PRT; 10 AA.  
 AC P82923;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).  
 GN MRPS2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=21276436; PubMed=11279123;  
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;  
 RT "The small subunit of the mammalian mitochondrial ribosome:  
 RT identification of the full complement of ribosomal proteins present.";  
 RL J. Biol. Chem. 276:19363-19374(2001).  
 CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit  
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.  
 DR InterPro; IPR001865; Ribosomal\_S2.  
 DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; PARTIAL.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON\_TER 1 1  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1246 MW; 6A7A6679C04B476B CRC64;

Query Match 19.1%; Score 17; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MEP 14  
 |||  
 Db 2 MEP 4

# RESULT 27

## HS70\_PINPS

ID HS70\_PINPS STANDARD; PRT; 11 AA.  
 AC P81672;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Heat shock 70 kDa protein (Fragment).  
 OS Pinus pinaster (Maritime pine).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=71647;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RX MEDLINE=99274088; PubMed=10344291;  
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Plomion C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins.";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein  
 CC (spot N164) is: 5.4, its MW is: 73 kDa.  
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.  
 KW ATP-binding; Heat shock; Multigene family.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 11;  
 Best Local Similarity 20.0%; Pred. No. 5.6e+03;  
 Matches 2; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 8 LQVMMEPQGD 17  
 :::: ||:  
 Db 1 VEIANDQGN 10

# RESULT 28

## TKNA\_GADMO

ID TKNA\_GADMO STANDARD; PRT; 11 AA.  
 AC P28498;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Gadus morhua (Atlantic cod).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.  
 OX NCBI\_TaxID=8049;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=92298992; PubMed=1376687;  
 RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A-related peptides from the brain  
 RT of the cod and trout.";  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S23306; S23306.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION (BY SIMILARITY).  
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 11;  
 Best Local Similarity 37.5%; Pred. No. 5.6e+03;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 PQPLLQVM 11  
 || : :|  
 Db 4 PQQFIGLM 11

#### RESULT 29

##### TKN1\_KASMA

ID TKN1\_KASMA STANDARD; PRT; 12 AA.  
 AC P08613;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hylambates kassinin ([Glu2,Pro5]kassinin).  
 OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;  
 OC Kassina.  
 OX NCBI\_TaxID=8414;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;  
 RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and  
 RT hylambatin, in the skin of the African rhacophorid frog Hylambates  
 RT maculatus.";  
 RL Biomed. Res. 2:613-617(1981).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S10059; S10059.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 12 12 AMIDATION.  
 SQ SEQUENCE 12 AA; 1376 MW; 3E756D279DD6DAB7 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 13 EPQGD 17  
 ||: |  
 Db 2 EPKPD 6

# RESULT 30

## ACT7\_SOYBN

ID ACT7\_SOYBN STANDARD; PRT; 13 AA.  
 AC P15987;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Actin 7 (Fragment).  
 GN SAC7.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Wayne;  
 RX MEDLINE=91346640; PubMed=2102831;  
 RA Pearson L., Meagher R.B.;  
 RT "Diverse soybean actin transcripts contain a large intron in the 5'  
 RT untranslated leader: structural similarity to vertebrate muscle actin  
 RT genes.";  
 RL Plant Mol. Biol. 14:513-526(1990).  
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved  
 CC in various types of cell motility and are ubiquitously expressed  
 CC in all eukaryotic cells.  
 CC -!- FUNCTION: Essential component of cell cytoskeleton; plays an  
 CC important role in cytoplasmic streaming, cell shape determination,  
 CC cell division, organelle movement and extension growth.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- MISCELLANEOUS: There are at least 16 actin genes in soybean.  
 CC -!- SIMILARITY: Belongs to the actin family.

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CC -----  
DR EMBL; X17120; CAA34980.1; -.  
DR PIR; S15755; S15755.  
DR InterPro; IPR004001; Actin.  
DR InterPro; IPR004000; Actin\_like.  
DR PROSITE; PS00406; ACTINS\_1; PARTIAL.  
DR PROSITE; PS00432; ACTINS\_2; PARTIAL.  
DR PROSITE; PS01132; ACTINS\_ACT\_LIKE; PARTIAL.  
KW Structural protein; Multigene family.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;

Query Match 19.1%; Score 17; DB 1; Length 13;  
Best Local Similarity 75.0%; Pred. No. 6.6e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLL 8  
|||:  
Db 8 QPLV 11

#### RESULT 31

##### LPAA\_PORGI

ID LPAA\_PORGI STANDARD; PRT; 13 AA.  
AC P81411;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Lipid-A-associated protein (Fragment).  
OS Porphyromonas gingivalis (Bacteroides gingivalis).  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Porphyromonadaceae; Porphyromonas.  
OX NCBI\_TaxID=837;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W50;  
RX MEDLINE=99061194; PubMed=9846737;  
RA Sharp L., Poole S., Reddi K., Fletcher J., Nair S., Wilson M.,  
RA Curtis M., Henderson B., Tabona P.;  
RT "A lipid A-associated protein of Porphyromonas gingivalis, derived  
RT from the haemagglutinating domain of the RI protease gene family, is  
RT a potent stimulator of interleukin 6 synthesis.";  
RL Microbiology 144:3019-3026(1998).  
CC -!- FUNCTION: IS ASSOCIATED WITH LIPID A, A PHOSPHORYLATED GLYCOLIPID  
CC THAT ANCHORS THE LIPOPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE  
CC CELL.  
FT VARIANT 12 12 G -> F.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1346 MW; 38EA796EAF63AB7 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QGD 17  
|||  
Db 2 QGD 4

RESULT 32

ECDC\_LYMDI

ID ECDC\_LYMDI STANDARD; PRT; 14 AA.  
AC P80940;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Testis ecdysiotropin peptide C (TE).  
OS Lymantria dispar (Gypsy moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Lymantriidae; Lymantria.  
OX NCBI\_TaxID=13123;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=97387807; PubMed=9243792;  
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,  
RA Bell R.A.;  
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a  
RT gonadotropin isolated from brains of Lymantria dispar pupae.";  
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).  
CC -!- FUNCTION: Stimulates synthesis of ecdysteroid in the testes of  
CC larvae and pupae.  
SQ SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;

Query Match 19.1%; Score 17; DB 1; Length 14;  
Best Local Similarity 75.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TPQP 6  
|||  
Db 8 TPLP 11

RESULT 33

ARCA\_STRP5

ID ARCA\_STRP5 STANDARD; PRT; 15 AA.  
AC P58827;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD)  
DE (Streptococcal acid glycoprotein) (Fragment).  
GN ARCA OR SAGP.  
OS Streptococcus pyogenes (serotype M5).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=160491;  
RN [1]

RP SEQUENCE, AND CHARACTERIZATION.  
 RC STRAIN=Manfredo / Serotype M5;  
 RX MEDLINE=98298018; PubMed=9632565;  
 RA Degnan B.A., Palmer J.M., Robson T., Jones C.E.D., Fischer M.,  
 RA Glanville M., Mellor G.D., Diamond A.G., Kehoe M.A., Goodacre J.A.;  
 RT "Inhibition of human peripheral blood mononuclear cell proliferation  
 RT by Streptococcus pyogenes cell extract is associated with arginine  
 RT deiminase activity.";  
 RL Infect. Immun. 66:3050-3058(1998).  
 CC -!- FUNCTION: Antitumor protein. Has a powerful and dose-dependent  
 CC inhibitory effect on antigen, superantigen, or mitogen-stimulated  
 CC human peripheral blood mononuclear cell (PBMC) proliferation. It  
 CC may inhibit cell proliferation by arresting cell cycle and  
 CC inducing apoptosis.  
 CC -!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).  
 CC -!- PATHWAY: Arginine degradation via arginine deiminase; first step.  
 CC -!- SUBUNIT: Homodimer.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -!- PTM: Glycosylated (By similarity).  
 CC -!- SIMILARITY: Belongs to the arginine deiminase family.  
 DR HAMAP; MF\_00242; -; 1.  
 KW Hydrolase; Arginine metabolism; Glycoprotein.  
 FT INIT\_MET 0 0  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1657 MW; D21150201B00EE46 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTP 4  
 |||  
 Db 3 QTP 5

#### RESULT 34

##### URE2\_MORMO

ID URE2\_MORMO STANDARD; PRT; 15 AA.  
 AC P17338;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Urease beta subunit (EC3.5.1.5) (15 kDa subunit) (Urea  
 DE amidohydrolase) (Fragment).  
 GN UREB.  
 OS Morganella morganii (Proteus morganii).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Morganella.  
 OX NCBI\_TaxID=582;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90264298; PubMed=2345135;  
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
 RT "Morganella morganii urease: purification, characterization, and  
 RT isolation of gene sequences.";  
 RL J. Bacteriol. 172:3073-3080(1990).  
 CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).

CC -!- SUBUNIT: (Alpha, beta, gamma)(3) (By similarity).  
CC -!- SIMILARITY: Belongs to the urease beta subunit family.  
DR PIR; B35389; B35389.  
KW Hydrolase.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1530 MW; 2D98944F2F20C7E8 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 15;  
Best Local Similarity 75.0%; Pred. No. 7.7e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PQPL 7  
| |  
Db 6 PTPL 9

#### RESULT 35

##### VORA\_METTM

ID VORA\_METTM STANDARD; PRT; 15 AA.  
AC P80907;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Ketoisovalerate oxidoreductase subunit vorA (EC 1.-.-.) (VOR) (2-  
DE oxoisovalerate oxidoreductase alpha chain) (2-oxoisovalerate-  
DE ferredoxin oxidoreductase alpha subunit) (Fragment).  
GN VORA.  
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
OC Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=79929;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=97261844; PubMed=9108258;  
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;  
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases  
RT in Methanobacterium thermoautotrophicum.";  
RL Eur. J. Biochem. 244:862-868(1997).  
CC -!- SUBUNIT: HETEROTRIMER OF THE VORA, VORB AND VORC SUBUNITS.  
CC -!- MISCELLANEOUS: Has a pH optimum of 9.7 and an optimal temperature  
CC of 75 degrees Celsius.  
KW Oxidoreductase.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1779 MW; 31320B6531CA528F CRC64;

Query Match 19.1%; Score 17; DB 1; Length 15;  
Best Local Similarity 30.0%; Pred. No. 7.7e+03;  
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQV 10  
:: | | :|  
Db 5 IRKPDSLXEV 14

#### RESULT 36

##### ACT6\_SOYBN

ID ACT6\_SOYBN STANDARD; PRT; 17 AA.

AC P15986;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Actin 6 (Fragment).  
 GN SAC6.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Wayne;  
 RX MEDLINE=91346640; PubMed=2102831;  
 RA Pearson L., Meagher R.B.;  
 RT "Diverse soybean actin transcripts contain a large intron in the 5'  
 RT untranslated leader: structural similarity to vertebrate muscle actin  
 RT genes.";  
 RL Plant Mol. Biol. 14:513-526(1990).  
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved  
 CC in various types of cell motility and are ubiquitously expressed  
 CC in all eukaryotic cells.  
 CC -!- FUNCTION: Essential component of cell cytoskeleton; plays an  
 CC important role in cytoplasmic streaming, cell shape determination,  
 CC cell division, organelle movement and extension growth.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- MISCELLANEOUS: There are at least 16 actin genes in soybean.  
 CC -!- SIMILARITY: Belongs to the actin family.  
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 CC -----  
 DR EMBL; X17119; CAA34979.1; -.  
 DR PIR; S15754; S15754.  
 DR InterPro; IPR004001; Actin.  
 DR InterPro; IPR004000; Actin\_like.  
 DR PROSITE; PS00406; ACTINS\_1; PARTIAL.  
 DR PROSITE; PS00432; ACTINS\_2; PARTIAL.  
 DR PROSITE; PS01132; ACTINS\_ACT\_LIKE; PARTIAL.  
 KW Structural protein; Multigene family.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 8.7e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLL 8  
 |||:  
 Db 8 QPLV 11

# RESULT 37

B29K\_PORGI

ID B29K\_PORGI STANDARD; PRT; 17 AA.  
AC P81784;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE 29 kDa immunogenic protein (Fragment).  
OS Porphyromonas gingivalis (Bacteroides gingivalis).  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Porphyromonadaceae; Porphyromonas.  
OX NCBI\_TaxID=837;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=VPB 3547;  
RX MEDLINE=20198497; PubMed=10731616;  
RA Norris J.M., Love D.N.;  
RT "Serum antibody responses of cats to soluble whole cell antigens of  
RT feline Porphyromonas gingivalis."  
RL Vet. Microbiol. 73:37-49(2000).  
KW Antigen.  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1756 MW; 383DE6AA14331AE0 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QGD 17  
|||  
Db 14 QGD 16

# RESULT 38

PC24\_BRANA

ID PC24\_BRANA STANDARD; PRT; 17 AA.  
AC P81097;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE 20 kDa pollen coat protein (Fragment).  
OS Brassica napus (Rape).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Brassica.  
OX NCBI\_TaxID=3708;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=cv. Topas; TISSUE=Pollen;  
RX MEDLINE=98345939; PubMed=9680961;  
RA Murphy D.J., Ross J.H.E.;  
RT "Biosynthesis, targeting and processing of oleosin-like proteins,  
RT which are major pollen coat components in Brassica napus."  
RL Plant J. 13:1-16(1998).  
CC -!- FUNCTION: Major component of the pollen coat.  
CC -!- TISSUE SPECIFICITY: Pollen.

CC -!- SIMILARITY: Belongs to the oleosin family.  
DR InterPro; IPR000136; Oleosin.  
DR PROSITE; PS00811; OLEOSINS; PARTIAL.  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 2018 MW; DC593833F02C52C9 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 8.7e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4  
||:  
Db 1 LQSP 4

#### RESULT 39

PSBL\_SYNVU

ID PSBL\_SYNVU STANDARD; PRT; 17 AA.  
AC P12241;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Photosystem II reaction center L protein (PSII 5 kDa protein)  
DE (Fragment).  
GN PSBL.  
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).  
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.  
OX NCBI\_TaxID=32053;  
RN [1]  
RP SEQUENCE.  
RA Ikeuchi M., Koike H., Inoue Y.;  
RT "Identification of psbI and psbL gene products in cyanobacterial  
RT photosystem II reaction center preparation.";  
RL FEBS Lett. 251:155-160(1989).  
CC -!- FUNCTION: Not known, it is however required for PSII activity.  
CC -!- SUBCELLULAR LOCATION: Cellular thylakoid membrane.  
CC -!- SIMILARITY: Belongs to the psbL family.  
DR PIR; S05033; S05033.  
DR HAMAP; MF\_01317; -; 1.  
DR InterPro; IPR003372; PSII\_PsbL.  
DR Pfam; PF02419; PsbL; 1.  
KW Photosynthesis; Thylakoid; Photosystem II; Reaction center.  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MEP 14  
|||  
Db 1 MEP 3

#### RESULT 40

HEX\_ADECU

ID HEX\_ADECU STANDARD; PRT; 18 AA.

AC P35985;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Hexon protein (Late protein 2) (Fragment).  
 GN PII.  
 OS Canine adenovirus type 1 (strain Utrecht).  
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
 OX NCBI\_TaxID=36364;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93033182; PubMed=1413543;  
 RA Cai F., Weber J.M.;  
 RT "Nucleotide and deduced amino acid sequence of the canine adenovirus  
 RT type 1 proteinase.";  
 RL Virus Genes 6:307-312(1992).  
 CC -!- FUNCTION: This protein is one of the structural proteins in the  
 CC viral coat and is synthesized during late infection.  
 CC -!- SUBUNIT: Homotrimer (By similarity).  
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 CC -----  
 DR EMBL; M72715; AAA42528.1; -.  
 DR PIR; A48550; A48550.  
 DR HSSP; P03277; 1DHX.  
 KW Coat protein; Hexon protein; Late protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 18 AA; 1938 MW; B9E2AE307A420962 CRC64;

Query Match 19.1%; Score 17; DB 1; Length 18;  
 Best Local Similarity 75.0%; Pred. No. 9.2e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4  
 |:|||  
 Db 7 LRTP 10

#### RESULT 41

##### NPMB\_BOVIN

ID NPMB\_BOVIN STANDARD; PRT; 8 AA.  
 AC P15507;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Morphine modulating neuropeptide B.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;

RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RX MEDLINE=86067985; PubMed=3865193;  
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;  
 RT "Isolation, sequencing, synthesis, and pharmacological  
 RT characterization of two brain neuropeptides that modulate the action  
 RT of morphine.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).  
 CC -!- FUNCTION: Modulates the action of morphine.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 DR PIR; B24749; B24749.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 18.0%; Score 16; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MMEPQ 15  
 : :||  
 Db 2 LFQPQ 6

#### RESULT 42

##### UF06\_MOUSE

ID UF06\_MOUSE STANDARD; PRT; 8 AA.  
 AC P38644;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familiar and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 5.2, its MW is: 50 kDa.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 18.0%; Score 16; DB 1; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 EPQG 16  
 |||  
 Db 3 EPGG 6

# RESULT 43

TKN\_PHYBI

ID TKN\_PHYBI STANDARD; PRT; 10 AA.  
AC P08610;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Phyllomedusin.  
OS Phyllomedusa bicolor (Two-colored leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Phyllomedusinae; Phyllomedusa.  
OX NCBI\_TaxID=8393;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=70267748; PubMed=5452018;  
RA Anastasi A., Erspamer G.F.;  
RT "Occurrence of phyllomedusin, a physalaemin-like decapeptide, in the  
RT skin of Phyllomedusa bicolor."  
RL Experientia 26:866-867(1970).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; S07202; S07202.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1189 MW; 3A257D7059D40457 CRC64;

Query Match 18.0%; Score 16; DB 1; Length 10;  
Best Local Similarity 30.0%; Pred. No. 7.4e+03;  
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVM 11  
| | : :|  
Db 1 QNPNRFIGLM 10

# RESULT 44

UPA2\_HUMAN

ID UPA2\_HUMAN STANDARD; PRT; 10 AA.  
AC P30088;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing."  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 4.4, its MW is: 49 kDa.  
 DR SWISS-2DPAGE; P30088; HUMAN.  
 FT NON\_TER 1 1  
 FT UNSURE 6 6  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;

Query Match 18.0%; Score 16; DB 1; Length 10;  
 Best Local Similarity 37.5%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 10 VMMEPQGD 17  
 | : | |  
 Db 1 VXLSPDD 8

#### RESULT 45

##### BPP3\_BOTIN

ID BPP3\_BOTIN STANDARD; PRT; 11 AA.  
 AC P30423;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom."  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; C37196; C37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 18.0%; Score 16; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQP 6  
| |:  
Db 2 LGPPRP 7

#### RESULT 46

##### NUDM\_CANFA

ID NUDM\_CANFA STANDARD; PRT; 12 AA.  
AC P54713;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE NADH-ubiquinone oxidoreductase 42 kDa subunit (EC 1.6.5.3)  
DE (EC 1.6.99.3) (Complex I-42KD) (CI-42KD) (Fragment).  
GN NDUFA10.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Heart;  
RX MEDLINE=98163340; PubMed=9504812;  
RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
RT dog heart proteins.";  
RL Electrophoresis 18:2795-2802(1997).  
CC -!- FUNCTION: Transfer of electrons from NADH to the respiratory  
CC chain. The immediate electron acceptor for the enzyme is believed  
CC to be ubiquinone.  
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
CC -!- COFACTOR: Binds 1 FAD per subunit.  
CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.  
CC This a component of the hydrophobic protein fraction.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
DR HSC-2DPAGE; P54713; DOG.  
KW Oxidoreductase; NAD; Ubiquinone; Flavoprotein; FAD; Mitochondrion.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1284 MW; 3CCD4E2B36EDD737 CRC64;

Query Match 18.0%; Score 16; DB 1; Length 12;  
Best Local Similarity 37.5%; Pred. No. 8.9e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 PLLQVMME 13  
|| :: |  
Db 5 PLAXILGE 12

# RESULT 47

TM2A\_METMA

ID TM2A\_METMA STANDARD; PRT; 12 AA.  
AC P80652;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit  
DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M  
DE methyltransferase 28 kDa subunit) (Fragment).  
OS Methanosarcina mazei (Methanosarcina frisia).  
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;  
OC Methanosarcinaceae; Methanosarcina.  
OX NCBI\_TaxID=2209;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;  
RX MEDLINE=96370840; PubMed=8774736;  
RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;  
RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:  
RT coenzyme M methyltransferase from Methanosarcina mazei Go1  
RT reconstituted in ether lipid liposomes."  
RL Eur. J. Biochem. 239:857-864(1996).  
CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN  
CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND  
CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-  
CC TETRAHYDROMETHANOPTERIN.  
CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-  
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-  
CC (methylthio)ethanesulfonate.  
CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match 18.0%; Score 16; DB 1; Length 12;  
Best Local Similarity 25.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QPLLQVMM 12  
:|:| :::  
Db 5 EPVLPLIV 12

# RESULT 48

CRBL\_ICASP

ID CRBL\_ICASP STANDARD; PRT; 13 AA.  
AC P17237;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Chemotactic peptide (I-CP).  
OS Icaria sp. (Ropalidian wasp).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Vespidae; Polistinae; Icaria.

OX NCBI\_TaxID=7495;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;  
 RL (In) Izumiya N. (eds.);  
 RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,  
 RL Osaka (1985).  
 CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 CC of neutrophils.  
 KW Mast cell degranulation; Chemotaxis; Amidation.  
 FT MOD\_RES 13 13 AMIDATION.  
 SQ SEQUENCE 13 AA; 1353 MW; 348DBC7AA30A3768 CRC64;

Query Match 18.0%; Score 16; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 9.6e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PLLQVM 11  
 ||| ::  
 Db 7 PLLGLL 12

#### RESULT 49

##### UN37\_CLOPA

ID UN37\_CLOPA STANDARD; PRT; 14 AA.  
 AC P81358;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Unknown protein CP 37 from 2D-page (Fragment).  
 OS Clostridium pasteurianum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=W5;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Flengsrud R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 RT sequence analysis of proteins from Clostridium pasteurianum W5."  
 RL Electrophoresis 19:802-806(1998).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.8, ITS MW IS: 44.7 kDa.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1579 MW; 05384662DEF89210 CRC64;

Query Match 18.0%; Score 16; DB 1; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 MEPQG 16  
 :| ||  
 Db 7 IEDQG 11

RESULT 50

COXI\_THUOB

ID COXI\_THUOB STANDARD; PRT; 15 AA.  
 AC P80978;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIc-2 (EC 1.9.3.1) (Fragments).  
 OS Thunnus obesus (Bigeye tuna).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
 OC Scombridae; Thunnus.  
 OX NCBI\_TaxID=8241;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=97454291; PubMed=9310366;  
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,  
 RA Kadenbach B.;  
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and  
 RT liver.";  
 RL Eur. J. Biochem. 248:99-103(1997).  
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide  
 CC chains of cytochrome c oxidase, the terminal oxidase in  
 CC mitochondrial electron transport.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 DR PIR; S77987; S77987.  
 KW Oxidoreductase; Inner membrane; Mitochondrion.  
 FT NON\_TER 1 1  
 FT NON\_CONS 8 9  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1696 MW; 4C4C966C73A40294 CRC64;

Query Match 18.0%; Score 16; DB 1; Length 15;  
 Best Local Similarity 37.5%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 10 VMMEPQGD 17  
 | :| |  
 Db 6 VAKKPMSD 13

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 Job time : 7.83582 secs